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g935.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2871>:

m935.seq

```

1  ATGTTGTATT TCAGATACGG CTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTCAGGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCAGATTGG
151 AAAGTTGAAA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTTCG CGACGCGCTC AACGGCAATC
251 AGGCGGATT AATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGGAAAGGCC GCGGAGGCGG TGGCGCGGTA TCGGGAAGT CACGGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCGGAGG CGGCAAAATT
501 GGATTTGCCG GCACCGGTTT TGGAAAATGT GGGGCGTTTT CGGAAAAAAA
551 CGGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC
601 AATAGAAATG CCAATAATGC CGCGCCGCAA TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCG GCCGGGCGGA GCGGGCGGCA GGGTTGAATT
701 ATGAAATCGA GCGGAAAAG CTGACGCCGT TGGCAGATAA TCATTATTTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTCA GTAAAAAATC
801 AGCTTATGAT GACGGGTTTCG GCAGGGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCG
901 GGCAGCGACG GCTTTGATGC GAAAACAAA CGGGTAAACA ACCGCCGCCT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCACTG TCCCATACTT
1001 ACCGCCCAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GCAGGCAGGA
1101 CGGGTTTTAT GTTTCGTTCG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTTGTG CGGTTTGTGC CGAAACGCGA AACGGTGGGC
1201 GCGCGGTCA ATAATGCCGC CTACCGGCGC AACGGTGTTC ATGCCGGTTG
1251 GCGCAGGAG TGGCGGCGAT TGGCGGTTT GAACAGTCGG GTTCCGCGT
1301 CTTATGCCCC CCGCAACTAT AAGGGCATTG CGGCTTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CGGCGTTGAA TTATCGTTTC GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACACGAGGT GTTTGTGTCG
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2872; ORF 935>:

m935.pep

```

1  MLYFRYGFLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51  KVENDAPRV DGDFLLAHPK MLEHSLRDAL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAAEFD
151 DFRKLSAERH FAEAAKLDLP APVLENVGRF RKKTEGLTGW RFSGGISPAV
201 NRNANNAAPQ YCRONGGRQI CSVSRAERAA GLNYEIEAEK LTPLADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDATK RVNRRRLPPY MLAGVGVQQL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFGGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAE WRQLGLNSR VSASYARRNY KGIAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPYA KRNSEVFVS
501 ADWRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2873>:

a935.seq

```

1  ATGTTGTATT TCAGATACGG TTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTCAGGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCGGATTGG
151 AAAGTTGACA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTTCG CGACGTGCTC AACGGCAATC
251 AGGCGGATTT GATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGGAAAGGCC GCGGAGGCGG TGGCGCGGTA TCGGGAAGT CACGGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCCGAGG CGGAAAAAAT
501 GGATTTGCCG GCGCCGTTTT TGGAAAATGT GGGGCGTTTT CGGAAAAAAG
551 CGGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC

```

1350

	310	320	330	340	350	360
m935.pep	GSDGFDKTKRVNNRRLPPYMLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
a935	GSDGFDKTKRVNNRRLPPYMLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
	310	320	330	340	350	360
	370	380	390	400	410	420
m935.pep	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPKRETVGGAVNNAAYRRNGVYAGWAQE					
a935	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPKRETVGGAVNNAAYRRNGVYAGWAQE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m935.pep	WRQLGGLNSRVSASYARRNYKGIAAFSTEAQRNREWNVSLALSHDKLSYKGIVPALNYRF					
a935	WRQLGGLNSRVSASYARRNYKGIAAFSTEAQRNREWNVSLALSHDKLSYKGIVPALNYRF					
	430	440	450	460	470	480
	490	500				
m935.pep	GRTESNVPYAKRRNSEVFVSADWRFX					
a935	GRTESNVPYAKRRNSEVFVSADWRFX					
	490	500				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2875>:

g936.seq

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51  CCTTGCCCTC GGCGGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
101 GCGCAAAATC CGTCATCGAC CGcgcgAACCA CCGgcgcgca AACCGATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCCGGT AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCGGGCGAC ATCGCCGGCG
401 ACACTTGGA CACGTCCAAA GTCCGCGCca cgCTGCTGGG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCaccgT CGGCGTACAA AAAGTCATTA CCCTCTACCA AAACCTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2876; ORF 936.ng>:

g936.pep

```

1  MKPKPHTVRT LIAAVLSLAL GGCFSVAVGG AAVGAKSVID RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHL LLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2877>:

m936.seq (partial)

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
51  CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGCGCGCA AACCGACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCCGGT AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCC...

```

This corresponds to the amino acid sequence <SEQ ID 2878; ORF 936>:

m936.pep (partial)

```

1  MKPKPHTVRT LIAAIFSLAL SGCVSAVIGS AAVGAKSAVD RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHL LLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTA...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 936 shows 93.8% identity over a 128 aa overlap with a predicted ORF (ORF 936.ng) from *N. gonorrhoeae*:

m936/g936

	10	20	30	40	50	60
m936.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAksAVDRRTTGAQTDDNVMALRIETT					
g936	MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAVGAksVIDRRTTGAQTDDNVMALRIETT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYLQNNQTKGYTPQISVVGYNRHL LLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
g936	ARSYLQNNQTKGYTPQISVVGYNRHL LLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	70	80	90	100	110	120
	130					
m936.pep	VASLPRTAXXX					
g936	VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2879>:

a936.seq

1	ATGAAACCCA	AACCGCACAC	CGTCCGCACC	CTGACTGCCG	CCGTCCTCAG
51	CCTTGCCCTC	GGCGGCTGCG	TCAGCGCAGT	CGTCGGCGGC	GCGGCGGTCTG
101	GCGCGAAATC	CGCCGTCGAC	CGCCGAACCA	CCGGCGCGCA	AACCGACGAC
151	AACGTAATGG	CGCTGCGTAT	CGAAACCACC	GCCCGCTCCT	ATCTGCGCCA
201	AAACAACCAA	ACCAAAGGCT	ACACGCCCCA	AATCTCCGTT	GTCGGCTACA
251	ACCGCCACCT	GCTGCTGCTC	GGACAAGTCG	CCACCGAAGG	CGAGAAACAG
301	TTCGTCGGTC	AGATTGCACG	TTCGGAACAG	GCCGCCGAAG	GCGTGTACAA
351	CTACATTACC	GTCGCCTCCC	TGCCGCGCAC	TGCCGGCGAC	ATCGCCGGCG
401	ACACTTGGAA	CACATCCAAA	GTCCGCGCCA	CGCTGTTGGG	CATCAGCCCC
451	GCCACACAGG	CGCGCGTCAA	AATCGTTACC	TACGGCAACG	TAACCTACGT
501	TATGGGCATC	CTCACCCCCG	AAGAACAGGC	GCAGATTACC	CAAAAAGTCA
551	GCACCACCGT	CGGCGTACAA	AAAGTCATCA	CCCTCTACCA	AAACTACGTC
601	CAACGCTGA				

This corresponds to the amino acid sequence <SEQ ID 2880; ORF 936.a>:

a936.pep

1	MKPKPHTVRT	LTA AVL SLAL	GGCVSAVVGG	AAVGAksAVD	RRTTGAQTDD
51	NVMALRIETT	ARSYLQNNQ	TKGYTPQISV	VGYNRHL LLL	GQVATEGEKQ
101	FVGQIARSEQ	AAEGVYNYIT	VASLPRTAGD	IAGDTWNTSK	VRATLLGISP
151	ATQARVKIVT	YGNVTYVMGI	LTPEEQAQIT	QKVSTTVGVQ	KVITLYQNYV
201	QR*				

m936/a936 95.3% identity in 128 aa overlap

	10	20	30	40	50	60
m936.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAksAVDRRTTGAQTDDNVMALRIETT					
a936	MKPKPHTVRTLTA AVL SLALGGCFSAVVGGAAVGAksAVDRRTTGAQTDDNVMALRIETT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYLQNNQTKGYTPQISVVGYNRHL LLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
a936	ARSYLQNNQTKGYTPQISVVGYNRHL LLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	70	80	90	100	110	120
m936.pep	VASLPRTA					

|||||||
a936 VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
130 140 150 160 170 180

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2881>:

g936-1.seq

```

1  ATGAAACCCA AACACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51  CCTTGCCCTC GCGGGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
101 GCGCAAAATC CGTCATCGAC CGcgaACCA CCGgcgcgca AACCGATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCGGGCGAC ATCGCCGGCG
401 ACACTTGGA CACGTCCAAA GTCCGCGCca cgCTGCTGGG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCaccgT CGGCGTACAA AAAGTCATTA CCCTCTACCA AAACCTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2882; ORF 936-1.ng>:

g936-1.pep

```

1  MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLLL GOVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2883>:

m936-1.seq

```

1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
51  CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCAGCAGC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG
401 ACACTTGGA CACATCCAAA GTCCGCGCCA CGCTGTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCACCGT CGGCGTACAA AAAGTCATCA CCCTCTACCA AAACCTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2884; ORF 936-1>:

m936-1.pep

```

1  MKPKPHTVRT LIAAIFSLAL SGCVSAVIGS AAVGAKSAVD RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLLL GOVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

m936-1/g936-1 95.5% identity in 202 aa overlap

	10	20	30	40	50	60
m936-1.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETT					
	: : : : : : : : :					
g936-1	MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAVGAAGSAVDRRTTGAQTDDNVMALRIETT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m936-1.pep	ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	: : : : : : : :					
g936-1	ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m936-1.pep	VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT					
	: : : : : : : :					

```
g936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT
              130      140      150      160      170      180
m936-1.pep      190      200
      QKVSTTVGVQKVITLYQNYVQRX
      |||||
g936-1      QKVSTTVGVQKVITLYQNYVQRX
              190      200
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2885>:

```
a936-1.seq
1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGACTGCCG CCGTCCTCAG
51  CCTTGCCCTC GCGGGCTGCG TCAGCGCAGT CGTCGGCGGC GCGGCGGTGC
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
151 AACGTAATGG CGCTGCGTAT CGAAACCACC GCCCGCTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAGGCT ACACGCCCCA AATCTCCGTT GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAGAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCCGCGAAG GCGTGTACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGCGC
401 ACACCTGGAA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCGC AAGAACAGGC GCAGATTACC CAAAAGTCA
551 GCACCACCGT CGGCGTACAA AAAGTCATCA CCCTCTACCA AACTACGTC
601 CAACGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2886; ORF 936-1.a>:

```
a936-1.pep
1  MKPKPHTVRT LTAAVLSLAL GCVSAVVG AAVGAKSAVD RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHL LLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIVT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*
```

a936-1/m936-1 97.0% identity in 202 aa overlap

```
m936-1.pep      10      20      30      40      50      60
      MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVD RRTTGAQTDD NVMALRIETT
a936-1      |||||
      MKPKPHTVRTLTAAVLSLALGCVSAVVGGAAVGAKSAVD RRTTGAQTDD NVMALRIETT
              10      20      30      40      50      60
m936-1.pep      70      80      90      100     110     120
      ARSYLRQNNQTKGYTPQISVVGYNRHL LLL GQVATEGEKQFVGQIARSEQAAEGVYNYIT
a936-1      |||||
      ARSYLRQNNQTKGYTPQISVVGYNRHL LLL GQVATEGEKQFVGQIARSEQAAEGVYNYIT
              70      80      90      100     110     120
m936-1.pep      130     140     150     160     170     180
      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
a936-1      |||||
      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
              130     140     150     160     170     180
m936-1.pep      190     200
      QKVSTTVGVQKVITLYQNYVQRX
a936-1      |||||
      QKVSTTVGVQKVITLYQNYVQRX
              190     200
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2887>:

```
g937.seq
1  atGAAAAATA TTCTCTTAgt ATTTGTTAGC TTTGTGCCAT TATGTGTCCG
51  CACTGATCTG CCGCTGAata tCGAAGACAT AATGaccgAC AAGGGAAAAT
101 GGAAactGGA AACTTccctt acctacctgA acaGCGAAAA cagCCGCGCC
151 GCACTTGCCT CACCGGTTTA CATTcAGACC GGCTCCGCTT CCTTTATCCC
201 CGTCCCGACC GAAATTCAGG AAAACGGCAG CAATACCGAT ATGCTCGCCG
251 GCACGCTCGG TTTGCGCTAC GGACTGaccg GCAataccgA CATTACGGC
301 AGCGGCAGCT ATCTGTGGCA CGAAGAACGC AAACTCGacg GCAACGGCAA
```

351	AACCCGCAAC	AAACGGATGT	CCGACATATC	CGCCGGCATC	AGCCACACCT
401	TCcttaAaGa	cgGCAAAAAT	CCCGCACTCA	TCGTTTTCCT	CGAAAGCACC
451	GTTTACGAAA	AATCGCGCAA	CAAAGCCTCG	TCGGGAAAAT	CGTGGTCATC
501	CGGCGCCACC	ACCTACAAAG	CCATAGATCC	GATTGTCTTT	TCCCTCACCG
551	CCGCTTACCG	CATCAACGGC	AGCAAAACCC	TTTCAGACGA	CGTCAAATAC
601	AAAGCAGGCA	ATTACTGGAT	GCTGAATCCC	AACATCTCAT	TTGCCGCCAA
651	CGACGGAATC	AGCCTGACCG	GAGGCATCCA	ATGGCTGGGC	AAACAGCCCC
701	ACCGCATAGA	CGGCAAAAAA	GAATCCGCAA	GAAACACATC	CACCTACGCC
751	CATTTTCGGC	CAGGTTTCGG	TTTCACCAAA	ACCGCGGCTT	TAAACGCATC
801	CGCACGTTTC	AACGTTTCAG	GGCAAAGCAG	TTCCGAAC TG	AAATTGGGCG
851	TACAGCATAC	ATTTTAA			

This corresponds to the amino acid sequence <SEQ ID 2888; ORF 937.ng>:
a937.pep

g937.pcp

1	<u>MKNILLVFS</u>	<u>FVPLCVRTL</u>	<u>PLNIEDIMTD</u>	<u>KGKWKLETSL</u>	<u>TYLNSENSRA</u>
51	<u>ALASPVYIQT</u>	<u>GSASFIPVPT</u>	<u>EIQENGSTND</u>	<u>MLAGTLGLRY</u>	<u>GLTGNTDIYG</u>
101	<u>SGSYLWHEER</u>	<u>KLDGNGKTRN</u>	<u>KRMSDISAGI</u>	<u>SHTFLKDGKN</u>	<u>PALIAFLEST</u>
151	<u>VYEKSRNKAS</u>	<u>SGKSLWIGAT</u>	<u>TYKAIDPIVL</u>	<u>SLTAAAYRING</u>	<u>SKTLSDDDVKY</u>
201	<u>KAGNYWMLNP</u>	<u>NISFAANDRI</u>	<u>SLTGGIQWLG</u>	<u>KQPRIDRGGK</u>	<u>ESARNTSTYA</u>
251	<u>HFGAGFGFTK</u>	<u>TAALNASARF</u>	<u>NVSGQSSSEL</u>	<u>KLGVQHTF*</u>	

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2889>:
m937.seq

m937.seq

1	ATGAAGCGCA	TCTTTTTTGCC	CGCCTTGCCC	GCCATCCTGC	CTTTATCCAC
51	TTATGCCGAC	CTGCCCTTGA	CGATTGAAGA	CATAATGACC	GACAAGGGAA
101	AATGGAAACT	GGAAACTTCC	CTTACCTACC	TGAACAGCGA	AAACAACCGC
151	GCCGAACCTG	CCGCACCGGT	TTACATTCAA	ACCGGCGCAA	CCTCGTTTAT
201	CCCCATTCCG	ACCGAAATCC	AAGAAAaCGG	CAGCAATACC	GATATGCTCG
251	TCGGCACGCT	CGGTTTTGCG	TACGGAAGT	CCGGGAATAC	CGACATTTAC
301	GGCAGCGGCA	GCTATCTGTG	GCACGAAGAA	CGCAAACTCG	ACGGCAACAG
351	CAAAACCCGC	AACAAACGGA	TGTCGACGT	ATCCCTCGGC	ATCAGCCACA
401	CTTTCCTTAA	AGACGACAAA	AACCCCGCCC	TAATCAGCTT	TCTTGAAAGC
451	ACGGTTTTAC	AAAAATCGCG	CAACAAAGCC	TCGTGCGGAA	AATCCTGGCT
501	CATCGGCGCC	ACCACCTACA	AAGCCATAGA	TCCGATTGTC	CTTTCCCTCA
551	CCGCCGCCTA	CCGCATCAAC	GGCAGCATAA	CCCTTTTACA	CGGCATCCGC
601	TACAAATCGG	GCAACTACCT	GCTGCTCAAC	CCCAACATCT	CATTGTGTCG
651	CAACGACAGA	ATCAGCCTGA	CCGGAGGCAT	CCAATGGCTG	GGCAGGCAGC
701	CCGACCCGAG	GGACGGCAAA	CGGGAATCCT	CCAGAAACAC	ATCCACCTAC
751	GCCCAATTCG	GCGCAGGTTT	CGGTTTCACC	AAAACCACGG	CTTTAAACGC
801	ATCCGACAGT	TTCAACGTTT	CAGGGCAAAG	CAGTTCCGAA	CTGAAATTGT
851	GCGTACAGCA	TACATTTTAA			

This corresponds to the amino acid sequence <SEQ ID 2890; ORF 937>:

m937.pcp..

1	<u>MKRIFLPALP</u>	<u>AILPLSTYAD</u>	<u>LPLTIEDIMT</u>	<u>DKGKWKLETS</u>	<u>LYTLNSENNRR</u>
51	<u>AELAAPVYIQ</u>	<u>TGATSFIP</u>	<u>TEIQENGST</u>	<u>DMLVGTGLR</u>	<u>YGLTGNTDIY</u>
101	<u>GSYSYLWHE</u>	<u>RKLDGNSKTR</u>	<u>NKRMSDVSLG</u>	<u>ISHTFLKDDK</u>	<u>NPALISFLES</u>
151	<u>TVYKSRNKA</u>	<u>SSGKSWLIGA</u>	<u>TTYKAIPIV</u>	<u>LSLTAAAYRIN</u>	<u>GSKTLSDGIR</u>
201	<u>YKSGNYLLLN</u>	<u>PNISFAANDR</u>	<u>ISLTGDIQWL</u>	<u>GRQPDRTDGK</u>	<u>RESSRNTSTY</u>
251	<u>AHFGAGFGFT</u>	<u>KTTALNASAR</u>	<u>FNVSGQSSE</u>	<u>LKFPVOHTF*</u>	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 937 shows 86.9% identity over a 289 aa overlap with a predicted ORF (ORF 937.ng) from *N. gonorrhoeae*:

g937/m937

```

          10           20           30           40           50           59
g937.pep MKNILL-VFVSFVPLCVRTDLP LNIEDIMTDKGKWKLETSLTYLNSENSRAALASPVYIQ
      || |:| :: :|| | : :||||:||||| ||||| ||||| ||||| ||||| :|| :|| :|| 
m937     MKRIFLPALPAILPLSTYADLP LTIEDIMTDKGKWKLETSLTYLNSEN NRAELAAPVYIQ
          10           20           30           40           50           60
          60           70           80           90          100          110          119
g937.pep TGSASFIPVPTEI QENGSNT DMLAGTLGLRYGLTG NTDI YGSGSYLWHEER KLDGN GKT
```



```

a937.seq
1 ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGC
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGCA
101 AATGGAACCT GGAACCTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACCTG CCGCACCGGT TTACATCCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCCG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCACGCT CGGTTTGGCG TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGCGA GCTATCTGTG GCACGAAGAA CGCAAACCTC ACGGCAACGG
351 CAAAACCCGA AACAAACCGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CCTTCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAAATCGC CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATCGA CCCCCTCGTC CTCTCATTGA
551 CCGCTGCCTA CCGTATCAAC GGCAGCAAAA CCCTTTCAAG CAACACCAAA
601 TACAAAGCAG GCAATTACTG GATGCTGAAT CCAATATATC CCTTCGCCGC
651 CAACGACAGA ATCAGCCTCA CGGGCGGCAT CCAATGGCTG GCGAAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTTC GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGACAGT TTCAACGTTT CAGGGCAAAG CAGTCCGAA CTGAAATTTG
851 GCGTACAGTA TACGTTTTAA

```

a937.pep

1	MKRIFLPALP	AILPLSAYAD	LPLTIEDIMT	DKGKWKLETS	LTYLNSENNRR
51	AELAAPVYIQ	TGATSFPIIP	TEIQENGST	DMLVGTGLRL	YGLTGNTDIY
101	GSGSYLWHEE	RKLDGNGKTR	NKRMSDVSLG	ISHTFLKDDK	NPALISFLES
151	TVYEKSRNKA	SSGSFWLIGA	TTYKAIDPVV	LSLTAAYRIN	GSKTSSNTK
201	YKAGNYWMLN	PNISFANDR	ISLTGGIQWL	GKQPDRLDGK	KESARNTSTY
251	AHFEGAGFGFT	KTTALNASAR	FNVSGQSSE	LKFGVQHTF*	

	10	20	30	40	50	60
m937.pep	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNAELAAPVYIQ					
a937	:					
	10	20	30	40	50	60
	MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNAELAAPVYIQ					
	70	80	90	100	110	120
m937.pep	TGATSFIPIPTEIQENGSDMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNSKTR					
a937	:					
	70	80	90	100	110	120
	TGATSFIPIPTEIQENGSDMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNGKTR					

1356

	130	140	150	160	170	180
m937.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a937	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m937.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a937	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLKGQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m937.pep	RESSRNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTEF					
a937	KESARNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTEF					
	250	260	270	280	290	

g939.seq not found yet

g939.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2893>:

m939.seq (partial)

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCCTCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATATCGG
201 CATCCGCGAC GTAAACGCAC CC...
```

This corresponds to the amino acid sequence <SEQ ID 2894; ORF 939>:

m939.pep (partial)

```

1  MKRLTLLAFV LAAGAVSASP KADVEKGQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD VNAP...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2895>:

a939.seq

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCATCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATATCGG
201 CATCCGCGAC GGTAAACGCA CCCACGGTTC GGCAGCTGTG ATGAAACCGG
251 TGGTAATGAA TTTGAGCGAT CAGGATATTT TGAACGTATC CGCATTCTAT
301 GCCAAACAGC AGCCCAAATC CCGTGAAGCC AATCCTAAGG AAAATCCCGA
351 ATTGGGTGCG AAAATCTATC GCGGCGGTTT GAGCGATAAA AAAGTGCCGG
401 CGTGTATGTC CTGCCACGGT CCGAGCGGTG CGGGTATGCC GGGGGCGGA
451 AGCGAAATTC AGGCTTATCC GCGTTTGGGC GGTCAGCATC AGGCATATAT
501 TGTGTAACAG ATGAATGCCT ACAAGTCCGG TCAGCGTAA AATACCATCA
551 TGGAAGATAT TGCAAACCGT ATGTCTGAAG AAGATTGAA AGCGGTCGCC
601 AACTTTATCC AAGGTTTGCG TTAA
```

This corresponds to the amino acid sequence <SEQ ID 2896; ORF 939.a>:

a939.pep

```

1  MKRLTLLAFV LAAGAVSASP KADVEKGQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD GKRTGHSAAV MKPVVMNLSQ QDILNVSAFY
101 AKQQPKSGEA NPKENPELGA KIYRGGLSDK KVPACMSCHG PSGAGMPGGG
151 SEIQAYPRLG GQHQAYIVEQ MNAYKSGQRK NTIMEDIANR MSEDLDKAVA
201 NFIQGLR*
```

m939/a939 100.0% identity in 70 aa overlap

	10	20	30	40	50	60
m939.pep	MKRLTLLAFVLAAGAVSASP KADVEKGQVAATVCAACHAADGNSGIAMYPRLAAQHTAY					
a939	MKRLTLLAFVLAAGAVSASP KADVEKGQVAATVCAACHAADGNSGIAMYPRLAAQHTAY					

1357

```

              10      20      30      40      50      60
              70
m939.pep      IYHQTIGIRDVNAP
              |||||
a939          IYHQTIGIRDGKRTHGSAAVMKPVVMNLSDDQDILNVSAFYAKQQPKSGEANPKENPELGA
              70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2897>:

```

g950.seq
1   ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
51  GGCCGCCGCGC GCCGTGCGCG CCCACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCAAAAATC CGCCCAAGGC TCTGCGGCG CATCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
201 TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
251 AAAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2898; ORF 950.ng>:

```

g950.pep
1   MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
51  SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA
101 EGKCGEGKCG SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2899>:

```

m950.seq
1   ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51  GGCCGCCGCGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2900; ORF 950>:

```

m950.pep
1   MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 950 shows 86.6% identity over a 112 aa overlap with a predicted ORF (ORF 950) from *N. gonorrhoeae*

m950/g950 86.6% identity in 112 aa overlap

```

              10      20      30      40      50
m950.pep      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----
              |||||
g950          MNKNIAAALAGALSLSLAAGAVAAHKPASNATGVQKSAQGSAGSCGASKSAEG
              10      20      30      40      50      60
              60      70      80      90      100
m950.pep      ----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
              |:|||||
g950          SCGAAASKAGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2901>:

```

a950.seq
1   ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51  GGCCGCCGCGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2902; ORF 950.a>:

a950.pep

```
1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 950 shows 100.0% identity over a 102 aa overlap with a predicted ORF (ORF 950) from *N. meningitidis*

a950/m950 100.0% identity in 102 aa overlap

```

      10      20      30      40      50      60
a950.pep MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG
          |||||
m950      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG
          |||||
      10      20      30      40      50      60

      70      80      90     100
a950.pep EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
          |||||
m950      EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
          |||||
      70      80      90     100
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2903>:

g951.seq

```
1 ATGATTATGT TACCCGCCCG TTTCACATATT TTATCTGTCC TCGCAGCAGC
51 CCTGCTTGCC GGACAGGCGT ATGCTGCCGG CGCGGCGGAT GTGGAGCTGC
101 CGAAGGAAGT CGGAAGGTT TTAAGGAAAC ATCGGCGTTA CAGCGAGGAA
151 GAAATCAAAA ACGAACGCGC ACGGCTTGCG GCAGTGGGCG AACGGGTCAA
201 CAGGGTGTTC ACGTGTGTTG GCGGTGAAAC GGCTTTGCAG AAAGGGCAGG
251 CGGGAACGGC TCTGGCAACC TATATGCTGA TGTTGGAACG CACAAAATCC
301 CCCGAAGTCG CCGAACGCGC CTTGGAATG GCCGTGTCGC TGAACCGGTT
351 TGAACAGGCG GAAATGATTT ATCAGAAATG GCGGCAGATC GAGCCTATAC
401 CGGGTGAGGC GCAAAAACGG GCGGGGTGGC TCGGAACGT ATTGAGGGAA
451 GGGGGAATC AGCATCTGGA CGGGTGGAAG GAGGTGCTGG CGCAATCGGA
501 CGATGTGCAA AAACGCAGGA TATTTTGTCT GCTGGTGCAA GCCGCCGTGC
551 AGCAGGGTGG GGTGGCTCAA AAAGCATCGA AAGCGGTTCC CCGTGCGGCG
601 TTGAAGTATG AACATCTGCC CGAAGCGGCG GTTGCCGATG CCGTGTTCGG
651 CGTACAGGGA CGCGAAAAGG AAAAGGCAAT CGAAGCTTTG CAGCGTTTGG
701 CGAAGCTCGA TACGGAATA TTGCCCCCA CTTTAATGAC GTTGCCTCTG
751 ACTGCACGCA AATATCCCGA AATACTCGAC GGCTTTTTCG AGCAGACAGA
801 CACCCAAAAC CTTTCGGCCG TCTGGCAGGA AATGGAATTT ATGAATCTGG
851 TTTCCCTGCG TAAGCCGGAT GATGCCATG CGCGTTTGAA CGTGCTGTTG
901 GAACACAACC CGAATGCAA CCGTATATTT CAGGCGGCGA TATTGGCGGC
951 AAACCGAAAA GAAGGTGCGT CCGTTATCGA CGGCTACGCC GAAAAGGCAT
1001 ACGGCAGGGG GACGGGGGAA CAGCGGGGCA GGGCGGCAAT GACGGCGGCG
1051 ATGATATATG CCGACCGCAG GGATTACGCC AAAGTCAGGC AGTGGTTGAA
1101 AAAAGTGTCC GCGCCGGAAT ACCTGTTGCA CAAAGGCGTG CTGCGCGCTG
1151 CGGCGGCTGC CGAATTGGAC GGAGGCCGGG CGGCTTTGCG GCAGATCGGC
1201 AGGGTGCGGA AACTTCCCGA ACAGCAGGGG CCGTATTTTA CGGCAGACAA
1251 TTTGTCCAAA ATACAGATGC TCGCCCTGTC GAAGCTGCCC GACAAACGGG
1301 AAGCCCTGAT CGGGCTGAAC AACATCATCG CCAAACCTTC GGCGCGGGGA
1351 AGCACGGAAC CTTTGGCGGA AGCATGGCA CAGCGTTCCA TTATTTACGA
1401 ACAGTTCGGC AAACGGGGAA AAATGATTGC CGACCTTGAA ACCGCGCTCA
1451 AACTTACGCC CGATAATGCA CAAATTATGA ATAATCTGGG CTACAGCCTG
1501 CTTTCCGATT CCAAACGTTT GGACGAGGTT TTCGCCCTGC TTCAGACGGC
1551 ATACCAAATC AACCCGGACG ATACCGCCGT TAACGACAGC ATAGGCTGGG
1601 CGTATTACCT GAAAGCGGAC GCGGAAAGCG CGCTGCCGTA TCTGCGGTAT
1651 TCGTTTGAAA ACGACCCCGA GCCCGAAGTT GCCGCCCAT TGGGCGAAGT
1701 GTTGTGGGCA TTGGGCGAAC GCGATCAGGC GGTGACGTA TGGACGAGG
1751 CGGCACACCT TAGGGGAGAC AAGAAAATAT GCGGGGAGAC GCTCAAACGC
1801 TACGGAATCG CCTTGCCCGA GCCTTCCCGA AAACCCCGGA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2904; ORF 951.ng>:

g951.pep

```
1 MIMLPARFTI LSVLAAALLA GQAYAAGAAD VELPKVGVK LKHHRYSEE
```

```
51 EIKNERARLA AVGERVNRVF TLLGGETALQ KGQAGTALAT YMLMLERTKS
101 PEVAERALEM AVSLNAFEQA EMIYQKWRQI EPIPGEAQKR AGWLRNVLRE
151 GGNQHL DGL E VLAQSD DVQ KRRIFLLLVQ AAVQGGVVAQ KASKAVRRRAA
201 LKYEHLPEAA VADAVFGVQG REKEKAIEAL QRLAKLDTEI LPPTLMTLRL
251 TARKYPEILD GFFEQTDTQN LSAVWQEMEI MNLVSLRKP DAYARLNVLL
301 EHNPNANLYI QAAI LAANRK EGASVIDGYA EKAYGRGTGE QRGRAAMTAA
351 MIYADRRDYA KVRQWLKQVS APEYLFDKGV LAAAAAEELD GGRAALRQIG
401 RVRKLPEQQG RYFTADNLSK IQMLALSCLP DKREALIGLN NIIAKLSAAG
451 STEPLAEALA QRSIIYEQFG KRGKMIADLE TALKLTPDNA QIMNNLGYSL
501 LSDSKRLDEG FALLQTAYQI NPDDTAVNDS IGWAYYLYKGD AESALPYLRY
551 SFENDPEPEV AAHLGEVLWA LGERDQAVDV WTQAAHLRGD KKIWRETLKR
601 YGIALPEPSR KPRK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2905>:

m951.seq

```
1 ATGATTATGT TACCTAACCG TTTCAAAATG TTAAGTGTGT TGACGGCAAC
51 CTTGATTGCC GGACAGGTAT CTGCCGCCGG AGGCGGTGCG GGGGATATGA
101 AACAGCCGAA GGAAGTCGGA AAGGTTTTCA GAAAGCAGCA GCGTTACAGC
151 GAGGAAGAAA TCAAAAACGA ACGCGCACGG CTTGCCGCGAG TGGGCGAGCG
201 GGTTAATCAG ATATTTACGT TGCTGGGAGG GGAACCCGCC TTGCAAAAGG
251 GGCAGGCGGG AACGGCTCTG GCAACCTATA TGCTGATGTT GGAACGCACA
301 AAATCCCCCG AAGTCGCCGA ACGCGCCTTG GAAATGGCCG TGTCGCTGAA
351 CGCGTTTGAA CAGGCGGAAA TGATTATCA GAAATGGCCG CAGATTGAGC
401 CTATACCGGG TAAGGCGCAA AACGGGCGG GGTGGCTGCG GAACGTGCTG
451 AGGGAAGAG GAAATCAGCA TCTGGACGGA CTGGAAGAAG TGCTGGCTCA
501 GGCAGACGAA GGACAGAAC GCAGGTGTT TTTATGTGTT GCACAAGCCG
551 CCGTGCAACA GGACGGGTTG GCGCAAAAG CATCGAAAGC GGTTCGCCGC
601 CGCGCGTTGA AATATGAACA TCTGCCCGAA GCGGCGGTTG CCGATGTGGT
651 GTTCAGCGTA CAGGACGCG AAAAGGAAA GGCAATCGGA GCTTTCAGC
701 GTTTGGCGAA GCTCGATACG GAAATATTGC CCCCCACTTT AATGACGTTG
751 CGTCTGACTG CACGCAAATA TCCGAAATA CTCGACGGCT TTTTCGAGCA
801 GACAGACACC CAAAACCTTT CGGCCGCTG GCAGGAAATG GAAATATGA
851 ATCTGGTTTC CCTGCACAGG CTGGATGATG CCTATGCGCG TTTGACGTG
901 CTGTTGGAAC GCAATCCGAA TGCAGACCTG TATATTCAGG CAGCGATATT
951 GCGGCAAAAC CGAAAAGAAG GTGCTTCCGT TATCGACGGC TACGCCGAAA
1001 AGGCATACGG CAGGGGACG GAGGAACAGC GGAGCAGGGC GCGGCTAACG
1051 GCGGCGATGA TGTATGCCGA CCGCAGGGAT TACGCCAAAG TCAGGCAAGT
1101 GCTGAAAAAA GTATCCGCGC CGGAATACCT GTTCGACAAA GGTGTGCTGG
1151 CCGCTGCGGC GGCTGTCGAG TTGGACGGCG GCAGGCGCGC TTTGCGGCG
1201 ATCGGCAGGG TGCGGAAACT TCCGAAACAG CAGGGGCGGT ATTTTACGGC
1251 AGACAATTG TCCAAAATAC AGATGCTCGC CCTGTCGAAG CTGCCCGATA
1301 AACGGGAGGC TTTGAGGGGG TTGGACAAGA TTATCGAAAA ACCGCTGCC
1351 GGCAGTAATA CAGAGTTACA GGCAGAGGCA TTGGTACAGC GGTCAAGTTG
1401 TTACGATCGG CTTGGCAAGC GGAATAAAT GATTTCAGAT CTTGAAAGGG
1451 CGTTGAGGCT TGCACCCGAT AACGCTCAGA TTATGAATAA TCTGGGCTAC
1501 AGCCTGCTGA CCGATTCCAA ACGTTTGAC GAAGGTTTCG CCCTGCTTCA
1551 GACGCGATAC CAAATCAACC CGGACGATAC CGCTGTCAAC GACAGCATAG
1601 GCTGGGCGTA TTACCTGAAA GGCAGCGCG AAAGCGCGCT GCCGTATCTG
1651 CGGTATTTCG TTGAAAACGA CCCCAGGCC GAAGTTGCCG CCCATTGGG
1701 CGAAGTGTG TGGGCATTGG GCGAACGCGA TCAGGCGGTT GACGTATGGA
1751 CGCAGGCGGC ACACCTTACG GGAGACAAGA AAATATGGCG GGAAACGCTC
1801 AAACGTCACG GCATCGCATT GCCCAACCT TCCGAAAAAC CTCGGAATA
1851 A
```

This corresponds to the amino acid sequence <SEQ ID 2906; ORF 791>:

m951.pep

```
1 MIMLPNRFKM LTVLTATLIA GOVSAAGGGA GDMKQPEVG KVFRKQORYS
51 EEEIKNERAR LAAVGERVNO IFTLLGGETA LQKGQAGTAL ATYMLMLERT
101 KSPEVAERAL EMAVSLNAFE QAEMIYQKWR QIEPIPGKAQ KRAGWLRNVL
151 RERGNQHL DGL LEEVLAQADE QNRRVFLLL AQAQVQDGL AQKASKAVRR
201 AALKYEHLPE AAVADVVSFV QGREKEKAIG ALQRLAKLDT EILPPTLMTL
251 RLRTARKYPEI LDGFFEQTDT QNLSAVWQEM EIMNLVSLHR LDDAYARLNV
301 LLERNPNADL YIQAAI LAAN RKEGASVIDG YAEKAYGRGT EEQRSRAALT
351 AAMMYADRRD YAKVRQWLKK VSAPEYLFDK GVLAAAAAVE LDGGRAALRQ
401 IGRVRKLPEQ QGRYFTADNL SKIQMLALS LKPDKREALRG LDKIIEKPPA
451 GSNTLQAEAL LVQRSVVYDR LGKRKKMISD LERAFRLAPD NAQIMNNLGY
501 SLLTDSKRLD EGFALLQTAY QINPDDTAVN DSIGWAYYLYK GDAESALPYL
551 RYSFENDPEP EVAHLGEVL WALGERDQAV DVWTQAAHLT GDKKIWRETL
601 KRHGIALPQP SRKPRK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 951 shows 88.6% identity over a 616 aa overlap with a predicted ORF (ORF 951) from *N. gonorrhoeae*

m951/g951 88.6% identity in 616 aa overlap

```
m951.pep      10      20      30      40      50      60
MIMLPNRFKMLTVLTATLIAGQVSAAGGGAGDMKQPKVEGKVFRRKQRYSEEEIKNERAR
g951          10      20      30      40      50
MIMLPARFTILSVLAAALLAGQAYAA--GAADVLPKEVGKVLKRRYSEEEIKNERAR

m951.pep      70      80      90     100     110     120
LAAVGERVNRQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE
g951          60      70      80      90     100     110
LAAVGERVNRVFTLLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE

m951.pep     130     140     150     160     170     180
QAEMIIYQKWRQIEPIPGKAQKRAQWLRNVLRRGNQHLDGLEEVLAQADEGQNRVFLLL
g951         120     130     140     150     160     170
QAEMIIYQKWRQIEPIPGEAQKRAQWLRNVLREGGNQHLDGLEEVLAQSDDVQKRIFLL

m951.pep     190     200     210     220     230     240
AQAAVQQDGLAQKASKAVRRAALKYEHLPAAVADVVFVSVQGREKEKAIGALQRLAKLDT
g951         180     190     200     210     220     230
VQAAVQQGGVAQKASKAVRRAALKYEHLPAAVADVVFVSVQGREKEKAIEALQRLAKLDT

m951.pep     250     260     270     280     290     300
EILPPTLMTLRLTARKYPEILDGFFEQTDTQNL SAVWQEMEIMNLVSLHRLDDAYARLNV
g951         240     250     260     270     280     290
EILPPTLMTLRLTARKYPEILDGFFEQTDTQNL SAVWQEMEIMNLVSLRKPDDAYARLNV

m951.pep     310     320     330     340     350     360
LLERNPNADLYIQAAILAANRKEGASVIDGYAEKAYGRGTGEEQSRRAALTAAMMYADRRD
g951         300     310     320     330     340     350
LLEHNPANLYIQAAILAANRKEGASVIDGYAEKAYGRGTGEEQSGRAAMTAAMIYADRRD

m951.pep     370     380     390     400     410     420
YAKVRQWLKQVSAPEYLFDKGVLA AAAA AVELDGGRAALRQIGRVRKLPEQQGRYFTADNL
g951         360     370     380     390     400     410
YAKVRQWLKQVSAPEYLFDKGVLA AAAA AVELDGGRAALRQIGRVRKLPEQQGRYFTADNL

m951.pep     430     440     450     460     470     480
SKIQMLALSKLPDKREALRGLDKIIEKPPAGSNTLQAEALVQSVVYDRLGKRKKMISD
g951         420     430     440     450     460     470
SKIQMLALSKLPDKREALIGLNNIIAKLSAAGSTEPLAEALAQRSIIEYQFGKRGKMIAD

m951.pep     490     500     510     520     530     540
LERAFRLAPDNAQIMNNLGYSLLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK
g951         480     490     500     510     520     530
LETALKLTPDNAQIMNNLGYSLLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK

m951.pep     550     560     570     580     590     600
GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL
g951         540     550     560     570     580     590
GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLRGDKKIWRETL

m951.pep      610
KRHGIALPQPSRKPRK
g951          600
KRYGIALPEPSRKPRKX
600      610
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2907>:

```
a951.seq
1  ATGTTACCCG CCCGTTTCAC CATTATCTCT GTGCTCGCGG CAGCCCTGCT
51  TGCCGGGGCAG GCGTATGCCG CCGGCGCGGC GGATGCGAAG CCGCCGAAGG
101 AAGTCGGAAA GGTTTTCAGA AAGCAGCAGC GTTACAGCGA GGAAGAAATC
151 AAAAACGAAC GCGCACGGCT TCGGCGAGTG GCGGAGCGGG TTAATCAGAT
201 ATTTACGTTG CTGGGAGGGG AAACCGCCTT GCAAAAGGGG CAGGCGGGAA
251 CGGCTCTGGC AACCTATATG CTGATGTTGG AACGCACAAA ATCCCCGAA
301 GTCGCCGAAC GCGCCTTGA AATGGCCGTG TCGCTGAACG CGTTTGAACA
351 GCGGGAATG ATTTATCAGA AATGGCGGCA GATTGAGCCT ATACCGGGTA
401 AGGCGCAAAA ACGGCGGGG TGGCTGCGGA ACGTGTCTAG GGAAGAGGA
451 AATCAGCATC TAGACGGACT GGAAGAAGTG CTGGCTCAGG CCGACGAAGG
501 ACAGAACCGC AGGGTGTTT TATTGTTGGC ACAAGCCGCC GTGCAACAGG
551 ACGGGTTGGC GCAAAAGCA TCGAAAGCGG TTCGCCGCGC GGCCTTGAGA
601 TATGAACATC TGCCCGAAGC GCGGTTGGC GATGTGGTGT TCAGCGTACA
651 GGGACGCGAA AAGGAAAAGG CAATCGGAGC TTTGCAGCGT TTGGCGAAGC
701 TCGATACGGA AATATTGCCC CCCACTTTAA TGACGTTGCG TCTGACTGCA
751 CGCAAATATC CCGAAATACT CGACGGCTTT TTCGAGCAGA CAGACACCCA
801 AAACCTTTTC GCCGCTCTGGC AGGAAATGGA AATTATGAAT CTGGTTTCCC
851 TGCACAGGCT GGATGATGCC TATGCGCGTT TGAACGTGCT GTTGAACGCG
901 AATCCGAATG CAGACCTGTA TATTCAGGCA GCGATATTGG CGGCAAAACCG
951 AAAAGAAGGT GCTTCCGTTA TCGACGGCTA CGCCGAAAAG GCATACGGCA
1001 GGGGGACGGG GGAACAGCGG GGCAGGCGCG CAATGACGGC GGCATGATA
1051 TATGCCGACC GAAGGGATTA CACCAAAATC AGGCAGTGGT TGAAGAAAGT
1101 GTCGCGCCCG GAATACCTGT TCGACAAAGG TGTGCTGGCG GCTGCGGCGG
1151 CTGTCTGAGT GGACGGCGGC AGGGCGGCTT TCGGCGAGAT CCGCAGGGTG
1201 CGGAAACTTC CCGAACAGCA GGGGCGGTAT TTACGGCAG ACAATTTGTC
1251 CAAAATACAG ATGTTGCCCC TGTCGAAGCT GCCCGACAAA CCGGAGGCTT
1301 TGAGGGGGTT GGACAAGATT ATCGAAAAAC CGCCTGCCGG CAGTAATACA
1351 GAGTTACAGG CAGAGGCATT GGTACAGCGG TCAGTTGTTT ACGATCGGCT
1401 TGGCAAGCGG AAAAAAATGA TTTCAGATCT TGAAGGGCGG TTCAGGCTTG
1451 CACCCGATAA CGCTCAGATT ATGAATAATC TGGGCTACAG CCTGCTTTCC
1501 GATTCCAAC GTTTGGACGA AGGCTTCGCC CTGCTTCAGA CGGCATACCA
1551 AATCAACCCG GACGATACCG CTGTCAACGA CAGCATAGGC TGGGCGTATT
1601 ACCTGAAAGG CGACGCGGAA AGCGCGCTGC CGTATCTGCG GTATTCTGTT
1651 GAAACGACCC CCGAGCCCGA AGTTGCGGCC CATTTGGGCG AAGTGTGTG
1701 GGCATTGGGC GAACGCGATC AGCGGTTGA CGTATGGACG CAGGCGGCAC
1751 ACCTTACGGG AGACAAGAAA ATATGGCGGG AAACGCTCAA ACGTCACGGC
1801 ATCGCATTGC CCCAACCTTC CCGAAACCT CGGAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2908; ORF 951.a>:

```
a951.pep
1  MLPARFTILS VLAALLAGO AYAAGAADAK PPKEVGKVFR KQORYSEEEI
51  KNERARLAIV GERVNQIFTL LGGETALQKG QAGTALATYM LMLERTKSPE
101 VAERALEMAV SLNAFEQAEM IYQKWRQIEP IPGKAQKRAG WLRNVLRERG
151 NQHLDEGLEEV LAQADEGQNR RVFLLAQAA VQODGLAQKA SKAVRRAALR
201 YEHLPEAAVA DVVFSVOGRE KEKAIGALQR LAKLDTEILP PTLMTLRLTA
251 RKYPEILDGF FEQTDTONLS AVWQEMEIMN LVSLHRLDDA YARLNVLLER
301 NPNADLYIQ AILAAANRKEG ASVIDGYAEK AYGRGTGEQR GRAAMTAAMI
351 YADRRDYTKV RQWLKKVSAP EYLFDKGVLA AAAAVELDGG RAALRQIGRV
401 RKLPEQQGRY FTADNLSKIQ MFALSKLPDK REALRGLDKI IEKPPAGSNT
451 ELQAEALVQR SVVYDRLGKR KKMISDLERA FRLAPDNAQI MNNLGYSLLS
501 DSKRLDEGFA LLQYAYQINP DDTAVNDSIG WAYYLGDAE SALPYLRYSF
551 ENDPEPEVAA HLGEVLWALG ERDQAVDVWT QAAHLTGDKK IWRETLKRHG
600 IALPQPSRKP RK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 951 shows 96.4% identity over a 614 aa overlap with a predicted ORF (ORF 951) from *N. meningitidis*

a951/m951 96.4% identity in 614 aa overlap

```

          10      20      30      40      50
a951.pep  MLPARFTILSVLAALLAGQAYAA--AADAKPPKEVGKVFRKQORYSEEEIKNERAR
          ||| || :||:|:|:|:|: ||| | :| | ||||| ||||| |||||
m951      MIMLPNRFKMLTVLTATLIAGQVSAAGGGAGDMKQPKVEGKVFRKQORYSEEEIKNERAR
          10      20      30      40      50      60
a951.pep  LAAVGERVNQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE
          60      70      80      90     100     110
```

```

|||||
m951      LAAVGERVNIQIFTLGGETALQKQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE
          70      80      90      100     110     120

          120     130     140     150     160     170
a951.pep  QAEMIQKWRQIEPIPGKAQKRAGWLRNVLRERGNQHLDGLEEVLAQADEGQNRVFLLL
          |||||
m951      QAEMIQKWRQIEPIPGKAQKRAGWLRNVLRERGNQHLDGLEEVLAQADEGQNRVFLLL
          130     140     150     160     170     180

          180     190     200     210     220     230
a951.pep  AQAAVQQDGLAQKASKAVRRAALRYEHLPEAAVADVVSQGREKEKAIGALQRLAKLDT
          |||||
m951      AQAAVQQDGLAQKASKAVRRAALRYEHLPEAAVADVVSQGREKEKAIGALQRLAKLDT
          190     200     210     220     230     240

          240     250     260     270     280     290
a951.pep  EILPPTLMTLRLTARKYPEILDGFFEOTDTQNL SAVWQEMEIMNLVSLHRLDDAYARLNV
          |||||
m951      EILPPTLMTLRLTARKYPEILDGFFEOTDTQNL SAVWQEMEIMNLVSLHRLDDAYARLNV
          250     260     270     280     290     300

          300     310     320     330     340     350
a951.pep  LLERNPNADLYIQAAILAANRKEGASVIDGYAEKAYGRGTGEQGRAAMTAAMIYADRRD
          |||||
m951      LLERNPNADLYIQAAILAANRKEGASVIDGYAEKAYGRGTEEQRSRAALTAAMMYADRRD
          310     320     330     340     350     360

          360     370     380     390     400     410
a951.pep  YTKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVRKLPEQQGRYFTADNL
          | : |||||
m951      YAKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVRKLPEQQGRYFTADNL
          370     380     390     400     410     420

          420     430     440     450     460     470
a951.pep  SKIQMFALSKLPDKREALRGLDKIIEKPPAGSNTELQAEALVQRSVVYDRLGKRKKMISD
          |||||
m951      SKIQMLALSKLPDKREALRGLDKIIEKPPAGSNTELQAEALVQRSVVYDRLGKRKKMISD
          430     440     450     460     470     480

          480     490     500     510     520     530
a951.pep  LERAFRLAPDNAQIMNNLGYSLLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK
          |||||
m951      LERAFRLAPDNAQIMNNLGYSLLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK
          490     500     510     520     530     540

          540     550     560     570     580     590
a951.pep  GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL
          |||||
m951      GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL
          550     560     570     580     590     600

          600     610
a951.pep  KRHGIALPQPSRKPRK
          |||||
m951      KRHGIALPQPSRKPRK
          610

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2909>:

g952.seq (partial)

```

1  ..TTGTCTTATC GTTTGAATGC TGCACCGATG TTTAACGATA ATCCTGTTGT
51  TTACGGAAAA ATCAAATGCG AGAGTTGGAA AGCGCGGCGG GATTTCAATA
101 TTGTAAAGCA GGATTGGAT TTTTCCTGCG GGGCGGCTTC GGTGGCGACG
151 CTTTTGAACA ATTTTACGG GCAAAAGCTG ACGGAAGAAG AAGTGTGGA
201 AAAACTGGGT AAGGAACAGA TGCGCGCGTC GTTTGAGGAT ATGCGGCGCA
251 TTATGCCCCG TTTGGGTTT GAGGCGAAAG GCTATGCCCT GTCTTTCGAA
301 CAGCTCGCGC AGTTGAAAAT CCCCCTCATC GTGTATCTGA AATACCGCAA
351 AGACGACCAT TTTTCGGTAT TGCGCGGAGT GGATGGCAAT ACGGTTTTCG
401 TTGCCGACCC GTCGCGGGT CATGTTTCGA TGAGCAGGGC GCAGTTTTTG
451 GAGGCTTGGC AAACCCGTGA GGGAAATTG GCAGGCAAAA TTTTGGCGGT
501 CGTGCCGAAA AAAGCGGAGG CGATTTCAAA TAAATGTTT TTCACACATC
551 ATCCCAAGCG GCAGACGGAG TTTGCAGTCG GACAGGTAAA ATGGTGGCGT

```


601 GCTTATTGA

This corresponds to the amino acid sequence <SEQ ID 2910; ORF 952.ng>:

g952.pep (partial)

```

1  ..LSYRLNAA PM FNDNPVVY GK IKLQSWKARR DFNIVKQDLD FSCGAASVAT
51  LLNIFYGQKL TEEEVLEKLG KEQMRASFED MRRIMPD LGF EAKGYALSFE
101 QLAQLKIPVI VYLKYRKDDH FSVLRGVDGN TVLLADPS PG HVMSMSRAQFL
151 EAWQTREGNL AGKILAVVPK KAEAISNKL F FTHHPKRQTE FAVGQVKWWR
201 AY*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2911>:

m952.seq

```

1  ATGATGAAGT TCAAATATGT TTTCTGTTG GCGTGTGTTG TCGTTTCTTT
51  ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
101 ACCGAAAAAT CAAAGTGCAG AGTTGGAAAG CGCGCGCGGA TTTCAATATT
151 GTAAAGCAGG ATTTGGATTT TTCTGTGGG GCGGCTTCGG TGGCGACGCT
201 TTTGAACAA TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTGAAAA
251 AGCTGGATAA GGAGCAGATG CGCGCGTCGT TTGAGGATAT GCGGCGCATT
301 ATGCCTGATT TGGGTTTTGA GGCGAAGGGC TATGCCCTGT CTTTCGAGCA
351 GCTCGCGCAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAAG
401 ACGACCATTT TTCGGTATTG CGCGGTATAG ACGGCAATAC GGTTTTGCTT
451 GCCGACCCGT CGCTGGGGCA TGTTCATG AGCAGGGCGC AGTTTTTGGA
501 TGCTTGGCAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCTGTCA
551 TACCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACAACAC
601 CCAAAACGGC AGACGGAGTT TACAGTCGGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2912; ORF 952>:

m952.pep

```

1  MMKFYVFL ACVVVLSYR LNAAPMFNDN PVVYGKIKVQ SWKARRDFNI
51  VKQDLDFSCG AASVATLLNN FYQTLTEEE VLKLDKEQM RASFEDMRRI
101 MPDLGF EAKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
151 ADPSLGHVSM SRAQFLDAWQ TREGNLAGKI LAVIPKKAET ISNKLFFTQH
201 PKRQTEFTVG QIRQARAE*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 952 shows 92.5% identity over a 201 aa overlap with a predicted ORF (ORF 952) from *N. gonorrhoeae*

g952/m952; 92.5% identity in 201 aa overlap

g952.pep	10	20	30	40
	LSYRLNAA PMFNDNPVVY GKIKLQSWKARRDFNIVKQDLDFSCG			
m952	10	20	30	40
	MMKFYVFLACVVVLSYRLNAA PMFNDNPVVY GKIKVQSWKARRDFNIVKQDLDFSCG			
g952.pep	50	60	70	80
	AASVATLLNIFYGQKL TEEEVLEKLGKEQMRASFEDMRRIMPD LGFEAKGYALSFEQLAQ			
m952	50	60	70	80
	AASVATLLNIFYGQTL TEEEVLEKLDKEQMRASFEDMRRIMPD LGFEAKGYALSFEQLAQ			
g952.pep	110	120	130	140
	LKIPVIVYLKYRKDDHFSVLRGVDGNTVLLADPS PGHVMSMSRAQFLEAWQTREGNLAGKI			
m952	110	120	130	140
	LKIPVIVYLKYRKDDHFSVLRGIDGNTVLLADPS LGHVMSMSRAQFLDAWQTREGNLAGKI			
g952.pep	170	180	190	200
	LAVVPKKAE AISNKLFFTHHPKRQTEFAVGQVKWWRAYX			
m952	170	180	190	200
	LAVIPKKAETISNKLFFTQHHPKRQTEFTVGQIRQARAE			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2913>:

a952.seq

```

1  ATGATGAAGT TCAAATATGT TTTCTGTTG GCGTGTGTTG TCGTTTCTTT
```

```

51  ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTGTTT
101  ACGGAAAAAT CAAAGTGCAG AGTTGGAAAG AAAGGCGGGA TTTCATATT
151  GTAAAGCAGG ATTTGGATTT TTCCTGCGGG GCGGCTTCGG TGGCGACGCT
201  TTTGAACAAT TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTGAAAA
251  AGCTGGATAA GGAGCAGATG CGCGCGTCGT TTGAGGATAT GCGGCGCATT
301  ATGCCAGATT TGGGTTTTGA AGCGAAAGGC TATGCCCTGT CTTTCGAGCA
351  GCTCGCACAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAGG
401  ATGATCATT CTGCGTATTG CGCGGGATAG ACGGCAATAC GGTTTTGCTT
451  GCCGACCCGT CGCTGGGTCA TGTTCGAATG AGCAGGGCGC AGTTTNGGA
501  TGCTTGGCAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCGGTCG
551  TGCCGAAAAA AGCCGAGACA ATTTCAAATA AATGTTTTT CACACATCAT
601  CCCAAGCGGC AGACGGAGTT TGCAGTCGGA CAAATCAGGC AAGCACGTGC
651  AGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2914; ORF 952.a>:

```

a952.pep
1   MMKFKYVELL ACVVVLSYSYR LNAAPMFNDN PVVYGKIKVQ SWKERRDFNI
51  VKODLDFSCG AASVATLLNN FYGQTLTEEE VLKKLDKEQM RASFEDMRRI
101 MPDLGFEEKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
151 ADPSLGHVSM SRAQFXDAWQ TREGNLAGKI LAVVPKKAET ISNKLFFTHH
201 PKRQTEFAVG QIRQARA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 952 shows 97.7% identity over a 218 aa overlap with a predicted ORF (ORF 952) from *N. meningitidis*

```

a952/m952    97.7% identity in 218 aa overlap

a952.pep      10      20      30      40      50      60
MMKFKYVELLACVVVLSYSYRLNAAPMFNDNPVVYGKIKVQSWKERRDFNIVKODLDFSCG
m952          10      20      30      40      50      60
MMKFKYVELLACVVVLSYSYRLNAAPMFNDNPVVYGKIKVQSWKARRDFNIVKODLDFSCG

a952.pep      70      80      90     100     110     120
AASVATLLNNFYGQTLTEEEVLKKLDKEQMRASFEDMRIMPDLGFEEKGYALSFEQLAQ
m952          70      80      90     100     110     120
AASVATLLNNFYGQTLTEEEVLKKLDKEQMRASFEDMRIMPDLGFEEKGYALSFEQLAQ

a952.pep     130     140     150     160     170     180
LKIPVIVYLKYRKDDHFSVLRGIDGNTVLLADPSLGHVSM SRAQFXDAWQTREGNLAGKI
m952         130     140     150     160     170     180
LKIPVIVYLKYRKDDHFSVLRGIDGNTVLLADPSLGHVSM SRAQFLDAWQTREGNLAGKI

a952.pep     190     200     210     219
LAVVPKKAETISNKLFFTHHPKRQTEFAVGQIRQARAEX
m952         190     200     210
LAVIPKKAETISNKLFFTHHPKRQTEFTVGQIRQARA*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2915>:

```

g953.seq
1   ATGAAAAAAA TCATCTTCGC CGCGCTCGCA GCGGCAGCCG TCGGCACTGC
51  CTCGCCACAC TACAAAGTGG ACGAATATCA CGCCAACGTC CGTTTCGCCA
101  TCGACCACTT CAACACCAGC ACCAACGTCG GCGGTTTTTA CGGTCTGACC
151  GGTTCGCTCG AGTTCGATCA AGCAAAACGC GACGGCAAAA TCGACATCAC
201  CATTCCCGTC GCCAACCTGC AAAGCGGTTT GCAACCCTTC ACCGCCACAC
251  TGAAATCCGC CGACATCTTC GATGCCGCTC AATATCCGGA CATCCGCTTC
301  GTTTCACCA AATTCAACTT CAACGGCAAA AAAGTTGTTT CCGTTGACGG
351  CAACCTGACC ATGCGCGGCA AAACCGCCCC CGTCAAACCT AAAGCCGAAA
401  AATTCAACTG CTACCAAAGC CCGATGGCGG AAACCGAAGT TTGCGGCGGC
451  GACTTCAGCA CCACCATCGA CCGCACCAAA TGGGCGGTGG ACTACCTCGT
501  TAACGCCGGT ATGACCAAAA ACGTCCGCAT CGACATCCAA ATCGAAGCTG
551  CAAAACAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2916; ORF 953.ng>:

g953.pep

```

1  MKKIIFAALA AAVGTASAT YKVDEYHANV RFAIDHFNTS TNVGGFYGLT
51  GSVVEFDQAKR DGKIDITIPV ANLQSGSQPF TGHLSADIF DAAQYPIRF
101 VSTKFNFNKG KLVSV DGNLT MRGKTAPVKL KAEKFNCYQS PMAETEVC GG
151 DFSTTIDRTK WGV DYL V NAG MTKNVRIDIQ IEAAKQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2917>:

m953.seq

```

1  ATGAAAAAAA TCATCTTCGC CGCACTCGCA GCCGCCGCCA TCAGTACTGC
51  CTCGCCCGCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCCCGTTTCG
101 CCATCGACCA TTTCAACACC AGCACCAACG TCGGCGGTTT TTACGGTCTG
151 ACCGGTTCCG TCGAGTTCTGA CCAAGCAAAA CGCGACGGTA AAATCGACAT
201 CACCATCCCC ATTGCCAACC TGCAAAGCGG TTCGCAACAC TTTACCGACC
251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC
301 TTTGTTTCCA CCAAATTCAA CTTCAACGGC AAAAACTGG TTTCCGTTGA
351 CGGCAACCTG ACCATGCACG GCAAAACCGC CCCCCTCAA CTCAAAGCCG
401 AAAAATTCAA CTGCTACCAA AGCCCGATGG AGAAAACCGA AGTTTGTGGC
451 GCGCACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT
501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
551 CAGCCAAACA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2918; ORF 953>:

m953.pep

```

1  MKKIIFAALA AAAISTASAA TYKVDEYHAN ARFAIDHFNT STNVGGFYGL
51  TGSVEFDQAK RDGKIDITIP IANLQSGSQH FTDHLKSADI FDAAQYPIR
101 FVSTKFNFNKG KLVSV DGNLT TMHGKTAPVK LKAEKFNCYQ SPMEKTEVCG
151 GDFSTTIDRT KWGM DYL V NV GMTKSVRIDI QIEAAKQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 953 shows 93.0% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. gonorrhoeae*

m953/g953 93.0% identity in 187 aa overlap

	10	20	30	40	50	60
m953.pep	MKKIIFAALAAAAAISTASAAATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAK					
g953	MKKIIFAALAAAAAVGTASA-TYKVDEYHANVRFAIDHFNTSTNVGGFYGLTGSVEFDQAK					
	10	20	30	40	50	
	70	80	90	100	110	120
m953.pep	RDGKIDITIPVIANLQSGSQHFTDHLKSADIFDAAQYPIRFVSTKFNFNKGKLVSV DGNL					
g953	RDGKIDITIPVIANLQSGSQPFTGHLKSADIFDAAQYPIRFVSTKFNFNKGKLVSV DGNL					
	60	70	80	90	100	110
	130	140	150	160	170	180
m953.pep	TMHGKTAPVKLKAKEKFNCYQSPMEKTEVC GDFSTTIDRTKWGM DYL V NV GMTKSVRIDI					
	:					
g953	TMRGKTAPVKLKAKEKFNCYQSPMAETEVC GDFSTTIDRTKWGV DYL V NAG MTKNVRIDI					
	120	130	140	150	160	170
m953.pep	QIEAAKQX					
g953	QIEAAKQX					
	180					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2919>:

a953.seq

```

1  ATGAAAAAAA TCATCATCGC CGCGCTCGCA GCAGCCGCCA TCGGCACTGC
51  CTCGCCCGCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCCCGTTTCT
101 CTATCGACCA TTTCAACACC AGCACCAACG TCGGCGGTTT TTACGGTCTG
151 ACCGGTTCCG TTGAGTTCTGA CCAAGCAAAA CGCGACGGTA AAATCGACAT
201 CACCATCCCC GTTGCCAACC TGCAAAGCGG TTCGCAACAC TTTACCGACC
251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC
301 TTTGTTTCCA CCAAATTCAA CTTCAACGGC AAAAACTGG TTTCCGTTGA

```

```

351 CGGCAACCTG ACCATGCACG GCAAAACCGC CCCCCTCAAA CTCAAAGCCG
401 AAAAATTCAG CTGCTACCAA AGCCCGATGT TGAAAACCGA AGTTTGCGGC
451 GCGCACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT
501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
551 CAGCCAAACA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2920; ORF 953.a>:

```

a953.pep
  1 MKKIIIAALA AAAIGTASAA TYKVDEYHAN ARFSIDHFNT STNVGGFYGL
  51 TGSVEFDQAK RDGKIDITIP VANLQSGSQH FTDHLKSADI FDAAQYPDIR
 101 FVSTKFNENG KKLVSVDGNL TMHGKTAPVK LKAEKFNCYQ SPMLKTEVCG
 151 GDFSTTIDRT KWGMDYLVNV GMTKSVRID I QIEAAKQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 953 shows 97.3% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. meningitidis*

a953/m953 97.3% identity in 187 aa overlap

```

a953.pep      10      20      30      40      50      60
               MKKIIIAALAAAIGTASAAATYKVDEYHANARFSIDHFNTSTNVGGFYGLTGSVEFDQAK
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m953          10      20      30      40      50      60
               MKKIIIFAALAAAISTASAAATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAK
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

a953.pep      70      80      90      100     110     120
               RDGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNENGKKLVSVDGNL
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m953          70      80      90      100     110     120
               RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNENGKKLVSVDGNL
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

a953.pep      130     140     150     160     170     180
               TMHGKTAPVKLKAEKFNCYQSPMLKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRID I
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m953          130     140     150     160     170     180
               TMHGKTAPVKLKAEKFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRID I
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

a953.pep      QIEAAKQX
               |||||
m953          QIEAAKQX

```

g954.seq not found yet

g954.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2921>:

```

m954.seq
  1 ATGAAAAAGT TTTATTTTGT GCTGCTGGCG TTGGGTTTGG CAGCGTGTGG
  51 GCAAGAACAA TCGCAGAAAG CTGATGCGGA GCAGTATTTT TTTGCCAATA
 101 AATATCAATT TGCAGATGAG AAACAGGCTT TTTATTTTGA ACGCGCCGCC
 151 CGTTTCCGTG TATTGCAACA AGGCCTTGGC GGGGATTTTG AGAGGTTTTT
 201 AAAAGGAGAA ATACCTAATC AAGAAAATCT TGCAAAGTAT CGTGAAAATA
 251 TTA CTCAAGC AGTCGCTTAT TATGCGGACA CGAATGGAGA TGATGACCCA
 301 TACCGCGTCT GCAAACAGGC TGCGCAAGAT GCAGAAATCC TGATGAAGAG
 351 TATGTAACA AGCGGTGGAG GCGGTACAAC TGATTAGAT AAGGAAAGTT
 401 ATCAAATTA CCGAAATCA ATGCAAGAAT GCCGTAAAC AATAACGGAA
 451 GCTGAAGCCA ATTTGCCGAA AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2922; ORF 954>:

```

m954.pep
  1 MKKFYFVLLA LGLAACGQEQ SOKADAEQYF FANKYQFADE KQAFYFERAA
  51 RFRVLQQLG GDFERFLKGE IPNQENLAKY RENITQAVAY YADTNGDDDP
 101 YRVCKQAAQD AEILMKSMVT SGGGGTTDLQ KESYQNYRKS MQECRKTITE
 151 AEANLPKK*

```

a954.seq not found yet

a954.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2923>:

g957.seq (partial)

1	ATGTTTAAAA	AATTCAAACC	GGTACTGTTG	TCATTTTTTG	CACTTGTATT
51	TGCCTTTTGG	CTGGGAACAG	GTATTGCCTA	TGAGATTAAT	CCGCGTTGGT
101	TTTTGAGCGA	TACGGCAACT	GAAGTACCTG	AAAATCCGAA	TGCTTTTGTG
151	GCGAAACTTG	CCCGCCTGTT	CCGAAATGCC	GACAGGGCGG	TTGTCACTCGT
201	GAAGGAATCG	ATGAGGACGG	AGGAAAGCCT	TGCCGGAGCT	GTGGATGACC
251	GTCCGTTGCA	GTCGGAGAAG	GATTATCTCG	CGCTCGCTAT	CCGGCTCAGT
301	CGTTTGAAAG	AAAAGGCGAA	ATGGTTTCAC	GTAACGGAGC	AGGAACATGG
351	GGAAGAGGTT	TGGCTGGATT	ACTATATCGG	CGAGGGCGGT	TTGGTTGCGG
401	TTTCGCTTTC	GCAACGCTCG	CCGGAAGCGT	TTGTTAATGC	CGAATATCTG
451	TATCGGAACG	ATCGTCCGTT	TTCTGTAAAT	GTGTACGGCG	GAACGGCTCA
501	CGGGGAAAAT	TATGAAACGA	CAGGAGAATA	TCGGGTTGTT	TGGCAACCGG
551	ACGGTTCGGT	ATTGATGCG	GCGGGGCGCG	GGAAAATCGG	GGAAGATGTT
601	TATGAGCATT	GCCTCGGGTG	TTATCAGATG	GCCCAGGTAT	ATTGGCGGAA
651	ATACCGGGAT	GTCGCGAATG	ACGAGCAGAA	GGTTTGGGAC	TTCCGCGAAG
701	AGAGCAACCG	GATTGCATCG	GACTCGCGCG	ATTATGTGTT	TTATCAGAAT
751	ATGCGGGAAT	TGATGCCCCG	GGGGatgaaG	gcgaacagtc	ttgtggtcgg
801	ctatgatgcg	gacggtCtgc	CgcaAAAagt	ctattggagt	gtcgacaatg
851	gaaaaaaacc	ccaaagtgtc	gaatattatt	tgaaaaacgg	aaatcttttt
901	attgcccaat	cttcgacggt	aaccttgaaa	acggatggcg	taacggcgga
951	tatgcaaacc	tatcatgcg	aacaaacgtt	gtatttggat	ggg...

This corresponds to the amino acid sequence <SEQ ID 2924; ORF 957.ng>:

g957.pep (partial)

1	MFKKFKPVLL	SFFALVFAPW	LGTGIAYEIN	PRWFLSDTAT	EVPENPNAPV
51	AKLARLFRNA	DRAVVIVKES	MRTEESLAGA	VDDGPLQSEK	DYLALAIRLS
101	RLKEKAKWFH	VTEQEHGEEV	WLDYYIGEGG	LVAVSLSQRS	PEAFVNAEYL
151	YRNDRPFVS	VYGGTAHGEN	YETTGEYRVV	WQPDGVSFDA	AGRGKIGEDV
201	YEHCLGICYQ	MQVYLAKYRD	VANDEQKVWD	FREESNRIAS	DSRDYVFYQN
251	MRELMPRGMK	ANSLVVGYYA	DGLPKQVYWS	VDNGKKPQSV	EYYLKNGNLF
301	IAQSSTVTLK	TDGVTADMQT	YHAQOTLYLD	G...	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2925>:

m957.seq

1	ATGTTTAAAA	AATTCAAACC	GGTACTGTTG	TCATTTTTTG	CACTTGTATT
51	TGCCTTTTGG	CTGGGAACGG	GTATTGCCTA	TGAGATTAAT	CCGCGTTGGT
101	TTTTGAGCGA	TACGGCAACT	GAAGTACCTA	AAAATCCGAA	TGCTTTTGTG
151	GCGAAACTTG	CCCGCCTGTT	CCGAAATGCC	GACAGGGCGG	TTGTCACTCGT
201	GAAGGAATCG	ATAAGGACGG	AGGAAAATCT	TGCCGGAACT	GTGGATGACG
251	GTCCGTTGCA	GTCGGAGAAG	GATTATCTCG	CGCTCGCTAT	CCGGCTCAGT
301	CGTTTGAAAG	AAAAGGCGAA	ATGGTTTCAC	GTAACGGAGC	AGGAACATGG
351	GAAAGAGGTT	TGGCTGGATT	ACCATATCGG	CGAGGGCGGT	TTGGTTGCGG
401	TTTCGCTTTC	GCAACGCTCG	CCGGAAGCAT	TTGTTAATGC	CGAATATCTG
451	TATCGGAACG	ATCGTCCGTT	TTCTGTAAAT	GTGTACGGCG	GAACGGTTCA
501	CGGGGAAAAT	TATGAAACGA	CAGGAGAATA	TCGGGTTGTT	TGGCAACCGG
551	ACGGTTCGGT	ATTGATGCG	GCGGGGCGCG	GGAAAATCGG	GGAAGATGTT
601	TATGAGCATT	GCCTCGGGTG	TTATCAGATG	GCCCAGGTAT	ATTGGCGGAA
651	ATACCGGGAT	GTCGCGAATG	ACGAGCAGAA	GGTTTGGGAC	TTCCGCAAAG
701	AGAGCAACCG	AATTGCGTGC	GACTCGCGCA	ATTCTGTGTT	TTATCAGAAT
751	ATGCGGGAAT	TGATGCCCCG	AGGGATGAAG	GCGAACAGTC	TTGTGGTCCG
801	CTATGATGCG	GACGGTCTGC	CGCAAAAAGT	CTATTGGAGT	TTTGACAATG
851	GAAAAAAACG	CCAGAGTTTC	GAATATTATT	TGAAAAACGG	AAATCTTTTT
901	ATTGCACAAT	CTTCGACGGT	AGCATTGAAA	GCGGATGGCG	TAACGGCGGA
951	TATGCAGACC	TATCATGCGC	AACAGACGTG	GTATTGGGAT	GGCGGGCGGA
1001	TTGTCCGCGA	AGAGAAACAG	GGAGACAGAC	TGCTTGATT	TCCTTTGAAC
1051	TTGGAAAATT	TGAAAAAGA	GGTGCGCCGT	TATGCAGAGG	CTGCGGCGAG
1101	ACGTTTCGGG	GGCAGGCGCG	ACCTTTCTCA	CTGA	

This corresponds to the amino acid sequence <SEQ ID 2926; ORF 957>:

m957.pep

1	MFKKFKPVLL	SFFALVFAPW	LGTGIAYEIN	PRWFLSDTAT	EVPKNPNAPV
51	AKLARLFRNA	DRAVVIVKES	IRTEENLAGT	VDDGPLQSEK	DYLALAIRLS
101	RLKEKAKWFH	VTEQEHGKEV	WLDYHIGEGG	LVAVSLSQRS	PEAFVNAEYL
151	YRNDRPFVS	VYGGTVHGEN	YETTGEYRVV	WQPDGVSFDA	AGRGKIGEDV
201	YEHCLGICYQ	MQVYLAKYRD	VANDEQKVWD	FRKESNRIAS	DSRNSVFYQN

251 MRELMPRGMK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYLLKNGNLF
 301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
 351 LENLEKEVRR YAEAAARRSG GRRDLSH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 957 shows 95.2% identity over a 331 aa overlap with a predicted ORF (ORF 957) from *N. gonorrhoeae*

g957/m957 95.2% identity in 331 aa overlap

g957.pep	10	20	30	40	50	60
m957	10	20	30	40	50	60
g957.pep	70	80	90	100	110	120
m957	70	80	90	100	110	120
g957.pep	130	140	150	160	170	180
m957	130	140	150	160	170	180
g957.pep	190	200	210	220	230	240
m957	190	200	210	220	230	240
g957.pep	250	260	270	280	290	300
m957	250	260	270	280	290	300
g957.pep	310	320	330			
m957	310	320	330	340	350	360
m957						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2927>:

a957.seq

```

1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGATT
51  TGCCTTTTGG CTGGAACCGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAATCCGA ATGCTTTTGT GGCGAAACTT
151 GCCCGCCTGT TCCGAAATGC CGACAGGGCG GTTGTTCATCG TGAAGGAATC
201 GATGAGGACG GAGGAAAGTC TTGCCGGAGC TGTGGATGAC GGTCCGTTGC
251 AGTCGGAGAA GGATTATCTT GCACTCGCTG TCCGGCTCAG TCGTTTGAAA
301 GAAAGGCGA AATGGTTTCA CGTAACGGAG CAGGAACATG GGAAGAGGT
351 TTGCTGCGAT TACTATATCG GCGAGGGCGG TTTGGTTGCG GTTTCGCTTT
401 CGCAACGCTC GCCGAAGCG TTTGTTAATG CCGAATATCT GTATCGGAAC
451 GATCGTCCGT TTTCTGTAAA TGTGTACGGC GGAACGGTTC ACGGGGAAAA
501 TTATGAAACG ACAGGAGAA ATCGGGTTGT TTGGCAACCG GACGGTTCGG
551 TATTTGATGC GTCGGGGCGC GGGAAATCG GGAAGATGT TTATGAGCAT
601 TGCTTCGGGT GTTATCAGAT GGCCAGGTA TATTGGCGA AATATCGGGA
651 TGTGCGAAT GATGAGCAGA AGGTTTGGGA CTTCCGCGAA GAGAGTAACC
701 GGATTGCGTC GGACTCGCGC GATTCTGTGT TTTATCAGAA TATGCGGGAA
751 TTGATGCCCC GAGGGATGAA GGCAAACAGT CTGTGGTCG GCTATGATGC
801 GGACGGTCTG CCGCAGAAAG TCTATTGGAG TTTCGACAA GGGAAAAAAC
851 GCCAGAGTTT CGAATATTAT TTGAAAAACG GAAATCTTTT TATTGCACAA
901 TCTTCGACGG TAGCATTGAA AGCGGATGGC GTAACGGCGG ATATGCAGAC

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951 CTATCATGCG CAACAGACGT GGTATTTAGA TGGCGGGCGG ATTGTCCGCG
1001 AAGAGAAACA GGGGGACAGA CTGCCTGATT TTCCTTTGAA CTTGGAAGAT
1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCCGG
1101 CGGCAGGCGC GACCTTTCTC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2928; ORF 957.a>:

```

a957.pep
1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
51  ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLYRN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGCVQMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
251 LMPRGMKANS LVVGYDADGL POKVYWSFDN GKKRQSFEYY LKNGNLFIAQ
301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
351 LEKEVSRYAE AAARRSGGRR DLSH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a957/m957 96.3% identity in 377 aa overlap

a957.pep	10	20	30	40	50
m957	10	20	30	40	50
a957.pep	60	70	80	90	100
m957	60	70	80	90	100
a957.pep	120	130	140	150	160
m957	120	130	140	150	160
a957.pep	180	190	200	210	220
m957	180	190	200	210	220
a957.pep	240	250	260	270	280
m957	240	250	260	270	280
a957.pep	300	310	320	330	340
m957	300	310	320	330	340
a957.pep	360	370			
m957	360	370			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2929>:

```

g958.seq
1  TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51  TTTCGGCAGC CATTGCGCCG CCGATACCGT TGCAGCGGAA GAGCGCGACC

```

```

101 GCGCTGTGCG AGAAGGCGGT GCGCAGGGCG CGTCCGAATC CGCACAAAGCT
151 TCCGATTTGA CCTCGGTTT GACCTGCCTG TTTTGCAGTA ACGAAAGCGG
201 CAGCCCCGAG AGAACCAGAG CCGCCGTCCA AGGCAGCGGC GAAGCATCCG
251 TCCCCGAAGA CTATACGCGC ATTGTTGCCG ACAGGATGGA AGGACAGTCG
301 AAGGTTAAGG TCGCGCGGGA AGGAAGCGTT ATCATCGAAC GGGACGGCGC
351 AGTCCTCAAT ACCGATTGGG CGGATTACGA CCAGTCGGGC GACACCGTTA
401 CCGTAGGCGA CCGGTTTCGCC CTCCAACAGG ACGGTACGCT GATTGCGGGC
451 GAAACCTGA CCTACAATCT CGATCAGCAG ACCGGCGAAG CGCACAACTG
501 CCGTATGGAA ACCGAACAAG GCGGACGGCG GCTGCAAAAG GTGAGCGGCA
551 CCGCCGAAAT GTTGGGCGAA GGGCGTTACA AACTGACGGA AACCCAATTC
601 AACACCTGTT CCGCCGGAGA TGCCGGCTGG TATGTCAAGG CCGCCTCTGT
651 CGAAGCCGAT CGGGGAAAAG GCATAGGCGT TGCCAAACAC GCCGCTTCG
701 TGTTCCGCGG CGTTCCCTTT TTCTATACGC CTGCGGCGGA CTTCCTCGTT
751 GACGGCAACG GCAAAAGCGG ACTGCTCGTC CCGTCCGTAT CTGCGGTTTC
801 GGACGGCGTT TCCCTTTCCG TCCCCTATTA TTTCAACCTT GCCCCCAACT
851 TCGATGCCAC TTTGCCCCC GGCATTATCG GCGAACGCGG CGCGACGTTT
901 GACGGACAAA TCCGTTACCT GCGTCCCGAT TACAGCGGAC AGACCGACCT
951 GACCTGGTTG CCGCACGATA AGAAAAGCGG CAGGAACAAC CGCTATCAGG
1001 CAAAATGGCA GCACCGGCAC GACATTCCG ACACGCTTCA GCGGGGTGTC
1051 GATTTCAACC AAGTCTCCGA CAGCGGCTAC TACCGCGACT TTTACGGCGG
1101 CGAAGAAATC GCGGCAACG TCAACCTCAA CCGCCGCGTA TGGCTGGATT
1151 ATGGCGGCGG GCGGCGGGA GGCAGCTGA ATGCCGGCCT TTCGGTTCAG
1201 AAATACCAGA CGTGGCAAA CCAAAGCGGC TACAAAGACG AACCTTACGC
1251 CATCATGCCC CGCCTTTCTG CCGATTGGCA TAAAAACGCA GGCAGGGCGC
1301 AAATCGGCGT GTCCGCACAA TTTACCCGCT TCAGCCACGA CGGCCGCCAA
1351 GACGGCAGCC GACTGGTCGT GTATCCCGGT ATCAAATGGG ATTTACAGCA
1401 CAGCTGGGGC TACGTCCGCC CCAAACCTCG GCTGCACGCC ACTTATTACA
1451 GCCTCGACAG TTTCCGCGGC AAAGCATCCC GCAGCGTCGG GCGCGTTTTG
1501 CCCGTTGTCA ATATCGACGG CGGCACAACC TTCGAACGCA ATACGCGCCT
1551 GTTCGCGCGG GGAGTCGTGC AAACCATCGA GCCGCGCCTG TTCTACAACT
1601 ATATTCTCTG CAAATCTCAA AACGACCTGC CCAATTTCTG TTCGTCGGAA
1651 AGCAGCTTCG GCTACGGGCA GCTTTTCCGC GAAAACCTCT ATTACGGCAA
1701 GCACCGCATC AACGCGGCCA ACAGCCTTTC CACCGCCGTG CAGAGCCGTA
1751 TTTTGGACGG CGCGACGGGG GAGGAGCGTT TCCGCGCCGG TATCGGTCAG
1801 AAATTTCTAT TCAAGGATGA TGCGGTGATG CTTGACGGCA GCGTCGGCAA
1851 AAATCCGCGC AGCCGTTCCG ACTGGGTGGC ATTGCGCTCC GCGGCGATAG
1901 GCGGGCGTTC CACCTCGAC AGCAGCATCC ACTACAACCA AAACGACAAA
1951 CCGGCCGAAC ATTACGCCGT CGGCGCAGGC TACCGCCCCG CCCCCGAAAA
2001 AGTGTGTAAG GCCCGCTACA AATACGGGCG CAACGAAAAA ATCTACCTGC
2051 AGGCGGACGG TTCTTATTTT TACGACAAAC TCAGCCAGCT CGACCTGTCC
2101 GCACAATGGC CGCTGACGCG CAACCTGTCT GCCGTCGTCC GCTACAACCTA
2151 CGGTTTTGAA GCCAAAAAAC CGATAGAAAT GCTTGCCGGT GCAGAATACA
2201 AAAGCAGTTG CGGCTGCTGG GCGCGGGGCG TGTACGCCCA ACGCTACGTT
2251 ACCGGCGAAA ACACCTACAA AAACGCCGTC TTTTTCCTAC TTCAGTTGAA
2301 AGACCTCAGC AGCGTCGGCA GAAACCCGCG AGGCAGGATG GATGTCGCGG
2351 TTCCCGGCTA CATCCCCGCC CACTCTCTTT CCGCCGGACG CAACAAACGG
2401 CCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2930; ORF 958.ng>:

g958.pep

```

1 LARLFSLKPL VLALGFCFGT HCAADTVAAE EADGRVAEGG AQGASESAQA
51 SDLTLGSTCL FCSNESGSPE RTEAAVQSGS EASVPEDYTR IVADRMEGQS
101 KVKVRAEGSV IIERDGAVALN TDWADYDQSG DTVTVGDRFA LQQDGTLRG
151 ETLYNLDDQ TGEAHNVME TEQGGRRLLQ VSRTAEMLGE GRYKLTETQF
201 NTCAGDAGW YVKAASVEAD RGKGIGVAKH AAFVFGGVPL FYTPWADFPL
251 DGNRKSGLLV PSVSAGSDGV SLSVPYYFNL APNFDATFAP GIIGERGATF
301 DGQIRYLPRD YSGQTDLTWL PHDKKSGRNN RYQAKWQHRH DISDTLQAGV
351 DENQVSDSGY YRDFYGGEEI AGNVNLNRRV WLDYGGRAAG GSLNAGLSVQ
401 KYQTLANQSG YKDEPYAIMP RLSADWHKNA GRAQIGVSAQ FTRFSDHGRQ
451 DGSRLVVYPG IKWDFSNSWG YVRPKLGLHA TYSLDSFSG KASRSVGRVL
501 PVVNIDGGTT FERNTRLFVG GVVQTIIEPRL FYNYPKASQ NDLPNFDSSE
551 SSFGYGLFR ENLYYGNDR NAANSLSTAV QSRILDGATG EERFRAGIGQ
601 KFYFKDDAVM LDGSVGKNPR SRSDWVAFAS GGIGGRFTLD SSIHYNQNDK
651 RAEHYAVGAG YRPAPGKVLN ARYKYGRNEK IYLOADGSYF YDKLSQLDLS
701 AQWPLTRNLS AVVRYNYGFE AKKPIEMLAG AEYKSSCGCW GAGVYAQRVY
751 TGENTYKNAV FFSLQLKDLS SVGRNPAGRM DVAVPGYIPA HSLSAGRNKR
801 P*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2931>:

m958.seq

```

1 TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTCTG
51 CTTCCGACAG CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGAA AGCGTTCGGA GCGTGTCCGA ACCCATAACG

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151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTTGCA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCGAAGCAT
251 CCATCCCCGA AGACTATACG CGCATTGTTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCGTCG AACGCAACCG
351 GACGACCCCTC AATACCGATT GGGCGGATTA CGACCACTCG GGCAGACCCG
401 TTACCGCAGG CGACCGGTTC GCCCTCCAAC AGGACGGTAC GCTGATTCCG
451 GGCGAAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGTCCGCATG GAAATCGAAC AAGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACTGAC GGAACCCAA
601 TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCAGCCTC
651 TGTCGAAGCC GATCGGAAAA AAGGCATAGG CGTTGCCAAA CACGCCGCCT
701 TCGTGTTCGG CGGCGTTCCC ATTTTCTACA CCCCTTGGGC GGAATCCCG
751 CTTGACGGCA ACCGCAAAAG CGGCCTGCTT GTTCCCTCAC TGTCCGCCGG
801 TTCGGACGGC GTTTCCCTTT CCGTTCCCTA TTATTTCAAC CTTGCCCCCA
851 ATCTCGATGC CACGTTCCGG CCCAGCGTGA TCGGCGAAGC CGGCGCGGTC
901 TTTGACGGC AGGTACGCTA CTTGCGGCCG GATTATGCCG GCCAGTCCGA
951 CCTGACCTGG CTGCCGCACG ACAAGAAAAG CGGCAGGAAT AACCGCTATC
1001 AGGCGAAATG CGAGCATCGG CACGACATTT CCGACACGCT TCAGGCGGGT
1051 GTCGATTTCG ACCAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATTATGGCGG CAGGGCGGCG GCGGCGACCC TGAATGCCGG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAGC GGCTACAAAG ACAAAACCGTA
1251 TGCCCTCATG CCGCGCCTTT CGGTGAGTGC GCGTAAAAAC ACCGGCAGGG
1301 CGCAATTCGG CGTGTCCGCA CAATTTACCC GATTACGCCA CGACAGCCGC
1351 CAAGACGGCA GCCGCCTGGT CGTCTATCCC GACATCAAAT GGGATTTTCA
1401 CAACAGCTGG GGCTATGTCC GTCCCAAAC CGGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAA GCGACGCGT CAGCCGCACT
1501 CTGCCCATTG TCAACATCGA CAGCGCGCGA ACTTTTGAGC GGAATACGCG
1551 GATGTTCCGG GGAGAAGTCC TGCAAACCT CGAGCCGCGC CTGTTCTACA
1601 ACTATATTCG TGCCAAATCC CAAAACGACC TGCCCAATT CGATTGCTCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTCTTT CGCGAAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCCGCC GTGCAAGGCC
1751 GTATTTTGGG CGGCGCGACG GGGGAAGAGC GTTCCGCGC CGGCATCGGT
1801 CAGAAATCTT ATTTCAAGGA TGATGCGGTG ATGCTTGACG GCAGCGTCGG
1851 CAAAAAACCG CGCAACCGTT CCGACTGGGT GGCATTTGCC TCCGGCAGCA
1901 TCGGCAGCCG CTTTCATCTC GACAGCAGCA TCCACTACAA CAAAAACGAC
1951 AAACGCGCCG AGAAGTACGC CGTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTGCTG AACGCCCGCT ACAAATACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCCTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAT GGCGCTGAC GCGCAACTCG TCGGCCGTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAGCAG TTGCGGCTGC TGGGCGCGCG GCGTGTACGC CCAACGCTAC
2251 GTTACCGCGC AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTGC GCAGAAACCC CGCAGACAGC ATGGATGTCG
2351 CCGTTCCCGG CTATATCACC GCCCACTCTC TTTCCGCCGG ACGCAACAAA
2401 CGACCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2932; ORF 958>:

m958.pep

```

1 LARLESLKPL VLALGLCFGT HCAADAVAA EETDNPTAGE SVRSVSEPIQ
51 PTSLSLGSTC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEOQ
101 SQQVRAEEN VVERNRRTL NTDWADYDQS GDTVTAGDRF ALQDGTLLIR
151 GETLTYNLEQ QTGEAHNVRM EIEQGGRRLO SVSRTAEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAVFEGGVP IFYTPWADFP
251 LDGNRKSGLL VPSLSAGSDG VLSVPPYFN LAPNLDATFA PSVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWOHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGS LNAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSVEWRKN TGRAQIGVSA QFTRFSDSR
451 QDGSRLVVYP DIKWDFSNSW GYVREPKLGLH ATYYSLNRFQ SOEARRVSRT
501 LPIVNIDSGA TFERNTRMFG GEVLQTLLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGQLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKDDAV MLDGSVGKPK RNRSDWVAFV SGISGRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGKVL NARYKYGRNE KIYLSKSDGSY FDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVLA GAEEKSSCGC WGAGVYAQRY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIT AHSLSAGRNK
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 958 shows 89.3% identity over a 802 aa overlap with a predicted ORF (ORF 958) from *N. gonorrhoeae*

m958/g958 89.3% identity in 802 aa overlap

```

      10      20      30      40      50      60
m958.pep  LARLFSLKPLVLALGLCFGTHCAAADAVAAEETDNPTAGESVRSVSEPIQPTSLSLGSTC
g958      LARLFSLKPLVLALGFCFGTHCAA-DTVAABEADGRVAEGGAQGAESDAQSDLTGSTC
      10      20      30      40      50
      70      80      90     100     110     120
m958.pep  LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTL
g958      LFCSNESGSPERTEAAVQGSGEASVPEDYTRIVADRMEGQSKVKVRAEGSVIIERDGAVL
      60      70      80      90     100     110
      130     140     150     160     170     180
m958.pep  NTDWADYDQSGDVTVTAGDRFALQQDGTLRGETLTYNLEQQTGEAHNVRMEIEQGGRRLO
g958      NTDWADYDQSGDVTVTGDRFALQQDGTLRGETLTYNLDQQTGEAHNVRMETEQGGRRLO
      120     130     140     150     160     170
      190     200     210     220     230     240
m958.pep  SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKGIGVAKHAAAFVGGVVP
g958      SVSRTAEMLGEGRYKLTETQFNTCSAGDAGWYVKAASVEADRGKGIGVAKHAAAFVGGVVP
      180     190     200     210     220     230
      250     260     270     280     290     300
m958.pep  IFYTFWADFPDGNRKSGLLVPSLSAGSDGVSLVSPYYFNLPNLDATFAPSVIGERGAV
g958      LFYTFWADFPDGNRKSGLLVPSVSAGSDGVSLVSPYYFNLPNFDATFAPGIIGERGAT
      240     250     260     270     280     290
      310     320     330     340     350     360
m958.pep  FDGQVRYLRPDYAGQSDLTWLPDHDKSGRNNRYQAKWQHRHDSITLQAGVDFNQVSDSG
g958      FDGQIRYLRPDYSGQDLDLTWLPDHDKSGRNNRYQAKWQHRHDSITLQAGVDFNQVSDSG
      300     310     320     330     340     350
      370     380     390     400     410     420
m958.pep  YYRDFYGNKEIAGNVNLRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM
g958      YYRDFYGGEEIAGNVNLRVWLDYGGRAAGGSLNAGLSVQKYQTLANQSGYKDEPYAIM
      360     370     380     390     400     410
      430     440     450     460     470     480
m958.pep  PRLSVEWRKNTGRAQIGVSAQFTREFSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH
g958      PRLSADWHKNAGRAQIGVSAQFTREFSHDGRQDGSRLVVYPGIKWDFSNSWGYVRPKLGLH
      420     430     440     450     460     470
      490     500     510     520     530     540
m958.pep  ATYYSLNRFGSQEARRVSRTLPIVNIDSGATFERNTRMFGGEVLQTLERLFYNYIPAKS
g958      ATYYSLDSFGGKASRSVGRVLPVVNIDGGTTFERNTRLFGGGVVQTIEPRLFYNYIPAKS
      480     490     500     510     520     530
      550     560     570     580     590     600
m958.pep  QNDLPNFDSSSESSFGYGQLFRENLYYGNDRINTANSLSAAVQSRILDGATGEERFRAGIG
g958      QNDLPNFDSSSESSFGYGQLFRENLYYGNDRINAANSLSTAVQSRILDGATGEERFRAGIG
      540     550     560     570     580     590
      610     620     630     640     650     660
m958.pep  QKFYFKDDAVMLDGSVGKPRNRSDWVAFASGSIGSRFILDSSIHYNQNDKRAENYAVGA
g958      QKFYFKDDAVMLDGSVGKNPRSRSDWVAFASGGIGGRFTLDSSIHYNQNDKRAEHYAVGA
      600     610     620     630     640     650
      670     680     690     700     710     720
m958.pep  SYRPAQGGKVLNARYKYGRNEKIYKSDGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF
g958      GYRPAQGGKVLNARYKYGRNEKIYQADGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF
      660     670     680     690     700     710
```

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              730      740      750      760      770      780
m958.pep      EAKKPIEVLGAIEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g958           EAKKPIEMLGAIEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPAGR
              720      730      740      750      760      770

              790      800
m958.pep      MDVAVPGYITAHSLSAGRNRKP
              |||||:|||||:|||||:|||||:
g958           MDVAVPGYIPAHSLSAGRNRKPX
              780      790      800

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2933>:

```

a958.seq
1   TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51  TTTCCGGCAG CATTGCGCCG CCGCCGATGC CGTTCGCGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGGA AGCGTTCGGA GCGTGTCCGA ACCCATACAG
151 CCTACCAGCC TGAGCCTCGG TCGACCTGC CTGTTTGTCA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCGGT CCAAGGCAGC GGCGAAGCAT
251 CCATCCCCGA AGACTATACG CGCATTGTGT CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCTGCG AACGCAATCG
351 GACGACCCCTC AATGCCGATT GGGCGGATTA CGACCACTGC GGCGACACCG
401 TTACCGCAGG CGACCGGTTC GCCCTCCAAC AGGACGGTAC GCTGATTCCG
451 GGCAGAAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGTCCGTATG GAAACCGAAC ACGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACCTGAC GGAAACCCAA
601 TTCAACACCT GTTCCGCCCG CGATGCCGCG TGGTATGTCA AGGCCGCTTC
651 CGTCGAAGCC GATCGGGAAG AAGGCATAGG CGTTGCCAAA CACGCCGCCCT
701 TCGTGTTCGG CGGCGTTCCC ATTTTCTACA CCCCTTGGGC GGAATTCCCG
751 CTTGACGGCA ACCGCAAAAG CGGCCTGCTC GTTCCCTCAC TGTCCGCCGG
801 TTCGGACGGC GTTTCCTTTT CCGTTCCTTA TTATTTCAAC CTGCCCCCA
851 ATCTCGATGC CAGTTCGCG CCGGCGTGA TCGGCGAAGC CGGCGCGGTC
901 TTTGACGGGC AGGTACGCTA CCTGCGGCCG GATTATGCCG GCCAGTCCGA
951 CCTGACCTGG CTGCCGCACG ACAAGAAAAG CGGCAGGAAT AACCGCTATC
1001 AGGCGAAATG GCAGCACCGG CACGACATTT CCGACACGCT TCAGGCGGGT
1051 GTCGATTTCA ACCAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATTATGGCGG CAGGCGGGCG GCGCGCAGCC TGAATGCCGG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAAGC GGCTACAAAG ACAAAACGTA
1251 TGCCCTGATG CCGCGCCTTT CCGCCGATTG GCGCAAAAAC ACCGGCAGGG
1301 CGCAATCCGG CGTGTCCGCC CAATTTACCC GCTTCAGCCA CGACAGCCGC
1351 CAAGACGGCA GCCGCTCGT CGTCTATCCC GACATCAAAT GGGATTTCAG
1401 CAACAGCTGG GGTACGTCC GTCCCAAACCT CGGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGTTCGGC AGCCAAGAAG CCCGACGCGT CAGCCGCACT
1501 CTGCCCATCG TCAACATCGA CAGCGCATG ACCTTCGAAG GCAATACGCG
1551 GATGTTCCGG GCGGAGTCC TGCAAACCTC CGAGCCGCGC CTGTTCTACA
1601 ACTATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTCTGCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTTTTT CGTGAAACCC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCCGCC GTGCAAAAGC
1751 GTATTTTGGG CGGCGCGACG GGGGAAGAGC GTTTCGCGCG CGGCATCGGG
1801 CAGAAATTCT ACTTCAAAAA CGACGCAGTC ATGCTTGACG GCAGTGTCGG
1851 CAAAAAACCG CGCAGCCGTT CCGACTGGGT GGCATTCGCC TCCAGCGGCA
1901 TCGGCAGCCG CTTTATCCTC GACAGCAGCA TCCACTACAA CCAAAACGAC
1951 AAACGCGCCG AGAACTACGC CGTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTGCTG AACGCCCGCT ACAAAATACG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCTTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAT GGCCGCTGAC GCGCAACCTG TCGGCGGTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCCAAAA AACCAGTAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAAGCAG TTGCGGCTGC TGGGGCGCGG GCGTGTACGC CCAACGCTAC
2251 GTTACCGGGC AAAACACCTA CAAAACGCT GTCTTTTCTC CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTGC GCAGAAACCC CGCAGACAGG ATGGATGTCG
2351 CCGTTCGCCG CTATATCCCC GCCCACTCTC TTTCCGCCGG ACGCAACAAA
2401 CGGCCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2934; ORF 958.a>:

```

a958.pep
1   LARLFSLKPL VLALGFCFGT HCAAADAVAA EETDNPTAGG SVRSVSEPIQ
51  PLSLSLSTC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEOQ
101 SQOVVRAEGN VVVERNRTTL NADWADYDQS GDTVTAGDRF ALQQDGLTIR
151 GETLTYNLEQ QTGEAHNVRM ETEHGGRRLL SVSRTEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAVFVGGVP IFYTPWADFP

```

```

251 LDGNRKSGLL VPSLSAGSDG VSLSVPPYFN LAPNLDATFA PGVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLRNR VWLDYGGRAA GGSLSNAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSADWRKN TGRAQIGVSA QFTRFSDHSR
451 QDGSRLVVYP DIKWDFSNSW GYVREPKLGLH ATYYSLNRFQ SQEARRVSR
501 LPIVNIDSGM TFERNTRMFG GGVLTQLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGOLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKNDV MLDGSVGKKP RSRSDWVAF SSGIGSRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGVK NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVL GA EYKSSCGC WGAGVYAQRY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIP AHSLSAGRNK
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a958/m958 98.1% identity in 802 aa overlap

a958.pep	10	20	30	40	50	60
	LARLFS	LKPLVL	LALGFC	FGTHCA	AAADAVA	AEETDN
m958	LARLFS	LKPLVL	LALGFC	FGTHCA	AAADAVA	AEETDN
	10	20	30	40	50	60
a958.pep	70	80	90	100	110	120
	LFCSNE	SGSPER	TEAAVQ	SGGEAS	IPEDYTR	IVADRM
m958	LFCSNE	SGSPER	TEAAVQ	SGGEAS	IPEDYTR	IVADRM
	70	80	90	100	110	120
a958.pep	130	140	150	160	170	180
	NADWAD	YDQSGD	TVTAGD	RFALQQ	DGTLIR	GETLT
m958	NTDWAD	YDQSGD	TVTAGD	RFALQQ	DGTLIR	GETLT
	130	140	150	160	170	180
a958.pep	190	200	210	220	230	240
	SVSRTA	EMLGEG	HYKLT	ETQFNT	CSAGDA	GWYVKA
m958	SVSRTA	EMLGEG	HYKLT	ETQFNT	CSAGDA	GWYVKA
	190	200	210	220	230	240
a958.pep	250	260	270	280	290	300
	IFYTPW	ADFP	LDGNRK	SGLLV	PVPSLS	AGSDGV
m958	IFYTPW	ADFP	LDGNRK	SGLLV	PVPSLS	AGSDGV
	250	260	270	280	290	300
a958.pep	310	320	330	340	350	360
	FDGQVR	YLRPD	YAGQSD	LTWLP	PHDKKS	GRNNRY
m958	FDGQVR	YLRPD	YAGQSD	LTWLP	PHDKKS	GRNNRY
	310	320	330	340	350	360
a958.pep	370	380	390	400	410	420
	YYRDFY	GNKEI	IAGNVN	LRNRV	WLDYGG	RAAGGS
m958	YYRDFY	GNKEI	IAGNVN	LRNRV	WLDYGG	RAAGGS
	370	380	390	400	410	420
a958.pep	430	440	450	460	470	480
	PRLSAD	WRKN	TGRAQI	GVSAQ	FTRFSD	HSRQDG
m958	PRLSAD	WRKN	TGRAQI	GVSAQ	FTRFSD	HSRQDG
	430	440	450	460	470	480
a958.pep	490	500	510	520	530	540
	ATYYSL	NRFSG	QEARRV	SRTLPI	VNIDSG	MTFERN
m958	ATYYSL	NRFSG	QEARRV	SRTLPI	VNIDSG	MTFERN

	490	500	510	520	530	540
a958.pep	550	560	570	580	590	600
m958	550	560	570	580	590	600
a958.pep	610	620	630	640	650	660
m958	610	620	630	640	650	660
a958.pep	670	680	690	700	710	720
m958	670	680	690	700	710	720
a958.pep	730	740	750	760	770	780
m958	730	740	750	760	770	780
a958.pep	790	800				
m958	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2935>:

g959.seq
 1 ATGAACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
 51 CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
 101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
 151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACCAG
 201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
 251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCCG
 301 GTGATTTCCT CCCGCCGCGA CGACTGA

This corresponds to the amino acid sequence <SEQ ID 2936; ORF 959.ng>:

g959.pep
 1 MNIKHLLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR
 51 AQAEKAARAR VGGKITDIDL EHDDGRPHYD VEIVKNGQEY KVVVDARTGR
 101 VISSRRDD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2937>:

m959.seq
 1 ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
 51 CATTTCCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
 101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
 151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCAG
 201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
 251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCCG
 301 GTGATTTCCT CCCGCCGCGA CGACTGA

This corresponds to the amino acid sequence <SEQ ID 2938; ORF 959>:

m959.pep
 1 MNIKHLLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
 51 AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
 101 VISSRRDD*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 959 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. gonorrhoeae*

m959/g959 95.4% identity in 108 aa overlap

	10	20	30	40	50	60
m959.pep	MNIKHL	LLTSAAT	LLSISAP	ALAHHD	GHGDD	DDHGHA
g959	MNIKHL	LLTAAAT	LLGISAP	ALAHHD	GHGDD	DDHGHA
	10	20	30	40	50	60

	70	80	90	100	109
m959.pep	VGGKIT	DIDLEH	DNGRPH	YDVEI	VKNQ
g959	VGGKIT	DIDLEH	DDGRPH	YDVEI	VKNQ
	70	80	90	100	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2939>:

a959.seq

```

1  ATGAACTTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
51  CATTTCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCAG
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2940; ORF 959.a>:

a959.pep

```

1  MNFKRLLTA AATALMGISA PALAHHDGHG DDDHGHAHQ HSKQDKIISR
51  AQAEEAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 959 shows 94.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. meningitidis*

a959/m959 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a959.pep	MNFKRLL	TAAATAL	MGISAP	ALAHHD	GHGDD	DDHGHA
m959	MNIKHL	LLTSAAT	LLSISAP	ALAHHD	GHGDD	DDHGHA
	10	20	30	40	50	60

	70	80	90	100	109
a959.pep	VGGKIT	DIDLEH	DNGRPH	YDVEI	VKNQ
m959	VGGKIT	DIDLEH	DNGRPH	YDVEI	VKNQ
	70	80	90	100	

g960.seq not found yet

g960.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2941>:

m960.seq

```

1  ATGCAAGTAA ATATTCAGAT TCCCTGTATG CTGTACAGAC GCGGGAGTGT
51  TAAGCCCCC TTGTTTGAAG CTCGCGGGCT CCTGCCGAGC TTCACCGACC
101 CCGTTGTGCC CAAGCTCTCT GCTCCCGGCG GCTACATTGT CGACATCCCC
151 AAAGGCAATC TGAAACCGA AATCGAAAAG CTGGCCAAAC AGCCCCAGTA
201 TGCCTATCTG AAACAGCTCC AAGTAGCGAA AAACGTCAAC TGGAAACAGG
251 TGCAACTGGC TTACGATAAA TGGGACTATA AGCAGGAAGG CTTAACCAGA
301 GCCGGTGCAG CGATTATCGC GCTGGCTGTT ACCGTGGTTA CTGCGGGCGC
351 GGGAGTCGGA GCCGCACTAG GCTTAAACGG CGCAGCCGCA GCAGCGGCCG
401 ATGCCGCTT TGCCTCACTC GCTTCTCAGG CTTCGGTATC GCTCATCAAC
451 AATAAAGGCG ATGTCGGCAA AACCCGTAAG GAACTGGGCA GAAGCCGCAC
501 GGTAAAAAAT CTGGTTGTAG CGCGGGCAAC GGCAGGCGTA TCCAACAAAC

```

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551 TCGGTGCTTC TTCCTTGCC ACTTGGAGCG AAACCCCTTG GGTAACAAC
601 CTCAACGTTA ACCTGGCCAA TCGGGGCGAGT GCCGCGCTGA TCAACACCGC
651 TGTTAACGGC GGCAGCCTGA AAGACAATCT GGAGGCAAT ATCCTGGCGG
701 CATTGGTGAA TACCGCGCAT GGGGAGGCGG CGAGTAAGAT CAAAGGACTG
751 GATCAGCACT ATGTCGCCCA CAAATCGCT CATGCGTAG CGGGCTGTGC
801 GGCTGCAGCG GCGAATAAGG GCAAATGTCA GGACGGCGCG ATCGGTGCGG
851 CTGTGGGTGA GATTGTGGG GAGGCTTTGG TTAAAATAC CGATTTTAGC
901 GATATGACCC CGGAACAATT AGATCTGGAA GTTAAGAAAA TTACCCCTTA
951 TGCCAACTT GCGGCAGGTA CAGTTGCAGG CGTAACGGGA GGAGATGTCA
1001 ATACTGCTGC ACAACCCGCA CAAACGCGG TAGAAAATAA TGCGGTTAAA
1051 GCTGTTGTAA CTGCTGCAAA AGTGGTTTAT AAGGTAGCCA GAAAAGGATT
1101 AAAAAACGGG AAAATCAACG TTAGAGATT AAAACAGACG TTGAAAGACG
1151 AAGGTTATAA TTTAGCCGAC AACCTGACCA CCTTATTCGA CGAAACATTG
1201 GATTGGAACG ATGCCAAAGC CGTTATTGAT ATTGTCGTCG GAACAGAGCT
1251 GAATCGCGCT AATAAGGGG AAGCGGCACA AAAGGTCAAG GAAGTTTtag
1301 AAAAAATCG TCCTTATATC CCTAATAAG GTGCTGTACC GAATATGAGT
1351 ACATACATGA AAAATAATCC TTTTGAAAA CAGCTGGCTC AAATTCAGA
1401 AAAGACAACG CTTCCGACGC AGCAAGGGCA GTCTGTCTTC TTGGTAAAAA
1451 GAAACCAAGG GTTATTAAAA ACCGGTGATA GGTTTATTT AGATGGCCAA
1501 CATAAAATC ATTTAGAGGT TTTTGATAA AATGGGAAC TTAAGTTTGT
1551 TCTAAATATG GATGGTTCGC TTAACCAAAT GAAACTGGG GCAGCAAAAG
1601 GTCGTAAATT AAACCTAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2942; ORF 960>:

```

m960.pep
1  MQVNIQIPCM LYRRGSVKPP LFEAPRLLPS FTDPVVPKLS APGGYIVDIP
51  KGNLKTIEK LAKOPEYAYL KQLQVAKNVN WNQVQLAYDK WDYKQEGLTR
101 AGAAIIALAV TVVTAGAGVG AALGLNGAAA AAADAFAFSL ASQASVSLIN
151 NKGDVGKTLK ELGRSRTVKN LVVAAATAGV SNKLGASSLA TWSETPWVNN
201 LNVNLANAGS AALINTAVNG GSLKDNLEAN ILAALVNTAH GEASKIKKL
251 DQHYVAHKIA HAVAGCAAAA ANKGKQDGA IGAAVGEIVG EALVKNTDFS
301 DMTPEQLDLE VKKITAYAKL AAGTVAGVTG GDVNTAAQTA QNAVENNAVK
351 AVVTAAKVVY KVARGLKNG KINVRDLKQT LKDEGYNLAD NLTLFDETL
401 DWNDAKVID IVVGTELNRA NKGEAAQVKV EVLEKNRPYI PNKGAVPNMS
451 TYMKNNPFGK QLAQISEKTT LPTQQGQSVF LVKRNQGLLK TGRFYLDGQ
501 HKNHLEVPDK NGNFKFVLMN DGSLNQMKTG AAKGRKLNK *

```

a960.seq not found yet

a960.pep not found yet

g961.seq not found yet

g961.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2943>:

```

m961.seq
1  ATGAGCATGA AACACTTTC AGCCAAAGTA CTGACCACAG CCATCCTTGC
51  CACTTTCTGT AGCGGCGCAC TGGCAGCCAC AAGCGACGAC GATGTTAAAA
101 AAGCTGCCAC TGTGGCCATT GTTGCTGCCT ACAACAATGG CCAAGAAATC
151 AACGGTTTCA AAGCTGGAGA GACCATCTAC GACATTGGTG AAGACGGCAC
201 AATTACCCAA AAAGACGCAA CTGCAGCCGA GTTGAAGCC GACGACTTAA
251 AAGGTCTGGG TCTGAAAAAA GTCGTGACTA ACCTGACCAA AACCGTCAAT
301 GAAAACAAAC AAAACGTCGA TGCCAAAGTA AAAGCTGCAG AATCTGAAAT
351 AGAAAAGTTA ACAACCAAGT TAGCAGACAC TGATGCCGCT TTAGCAGATA
401 CTGATGCCGC TCTGGATGAA ACCACCAACG CCTTGAATAA ATTGGGAGAA
451 AATATAACGA CATTGCTGTA AGAGACTAAG ACAAATATCG TAAAAATTGA
501 TGAAAAATTA GAAGCCGTGG CTGATACCGT CGACAAGCAT GCCGAAGCAT
551 TCAACGATAT CGCCGATTCA TTGGATGAAA CCAACACTAA GGCAGACGAA
601 GCCGTCAAAA CCGCAATGA AGCCAAACAG ACGGCCGAAG AAACCAACAA
651 AAACGTCGAT GCCAAAGTAA AAGCTGCAGA AACTGCAGCA GGCAAAAGCCG
701 AAGCTGCCGC TGGCAGAGCT AATACTGCAG CCGACAAGGC CGAAGCTGTC
751 GCTGCAAAAG TTACGACAT CAAAGCTGAT ATCGCTACGA ACAAAGCTGA
801 TATTGCTAAA AACTCAGCAC GCATCGACAG CTTGGACAAA AACGTAGCTA
851 ATCTGCGCAA AGAAACCCGC CAAGGCTTTC CAGAACAAGC CGCGCTCTCC
901 GGCCTGTTC AACCTTACAA CGTGGGTCGG TTCAATGTAA CGGCTGCAGT
951 CGCGGCTAC AAATCCGAAT CGGCAGTCGC CATCGGTACC GGCTTCCGCT
1001 TTACCGAAAA CTTTGCCGCC AAAGCAGGCG TGGCAGTCGG CACTTCGTCC
1051 GGTCTCTCCG CAGCCTACCA TGTGCGCGTC AATTACGAGT GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 2944>:

```

m961.pep
1  MSMKHFPKLV LTTAILATFC SGALAATSDD DVKKAATVAI VAAAYNNQOEI

```

```

51  NGFKAGETIY DIGEDGTITQ KDATAADVEA DDFKGLGLKK VVTNLTKTVN
101 ENKQNVDAKV KAAESEIEKL TTKLADTDAA LADTDAALDE TTNALNKLGE
151 NITTFAEETK TNIVKIDEKL EAVADTVDKH AEA FN DIADS LDETNTKADE
201 AVKTANEAKQ TAEETKQNV D AKVKAETA A GKAEAAAGTA NTAADKAEAV
251 AAKVTDIKAD IATNKADIAK NSARIDSLDK NVANLRKETR QGLAEQAALS
301 GLFQPNVGR FNVTAAGGY KSESAVAIGT GFRFTENFAA KAGVAVGTSS
351 GSSAAYHVG V NYEW*

```

a961.seq not found yet
a961.pep not found yet

g972.seq not found yet
g972.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2945>:

```

m972.seq
1  TTGACTAACA GGGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATCCG CAGCGAAGAG GTAAGCAAGA CggGGTTTTT
151 GTTGATTGGA TTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA
251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATGTTGA
351 TTATGGAGAG GTGCATTCG GArGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTGTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCACGATAA TGTTTGTGAT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGCGG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTTGT TCGTGTATAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAGAA AGCAAATGGG TAAGGTTCTGA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCGAAAG GTTTGATCAG AGAAAGAAAA AGCTTAATTT AACTTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTTTAT
951 GATTGAAATG GTTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAAGGCAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAAATT GAACCTGATG AATTGGGGGT TATTGCTTTT AAAAATTCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTTA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAATGT
1251 AGATTATGAT TATTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2946; ORF 972>:

```

m972.pep
1  LTNRGGAKLK TXSKSSERMS EVEYFSHFIS DGKGKLEIP ORRGKQDGVF
51  VDWISETFHE DTLKVS GCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHFGXQRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RTITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNED GSGKTFYVGR KNSRFRVRY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFPICRKF NMPVPERFDQ RKKKLNLTFE
301 HKLHYAKNAV GKLVNFMIE M GFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKQYEYLS KVYHQNVDDYD YF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2947>:

```

a972.seq
1  TTGACTAACA GGGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATCCG CAGCGAAGAG GTAAGCAAGA CGGGGTTTTT
151 GTTGATTGGA TTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA

```


1379

```
251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTTCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTTC GAGGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTTTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACCATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTTGT TCGTGTATAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAAGAA AGCAAATGGG TAAGGTTCTGA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCGAAG GTTTGATCAG AGAAAGAAAA CGCTTAATTT AACTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTTTAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAAGGCAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAAATG
1051 TTAAGGGACG GTTGAAACA CGTTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAAATT GAACTTGATG AATTGGGGGT TATTGCTTTT AAAAATTCG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTGA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAATGT
1251 AGATTATGAT TATTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2948; ORF 972.a>:

```
a972.pep
  1 LTNRGGAKLK TNSKSSERMS EVEYFSHFIS DGK GKLEIP QRRGKQDGVF
 51 VDWISFTFHE DTLLKVSGCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDDVDYGE VHF GGQRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RTITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNE DSGKTFYVGR KKNRFRVRY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFFICRKFK NMPVPERFDQ RKKTNLNLTFE
301 HKLHYAKNAV GKLVNFMIE MFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKQYEYLS KVVHQNVDDYD YF*
```

m972/a972 99.3% identity in 422 aa overlap

```

      10      20      30      40      50      60
m972.pep LTNRGGAKLKTXXSKSSERMSEVEYFSHFISDGK GKLEIPQRRGKQDGVFVDWISFTFHE
      |||
a972      LTNRGGAKLKTNSKSSERMSEVEYFSHFISDGK GKLEIPQRRGKQDGVFVDWISFTFHE
      10      20      30      40      50      60

      70      80      90     100     110     120
m972.pep DTLLKVSGCPLFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDDVDYGE
      |||
a972      DTLLKVSGCPLFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDDVDYGE
      70      80      90     100     110     120

      130     140     150     160     170     180
m972.pep VHF GGQRNTVLVELKGTGCSVASPGWELRLKQFLDDSI RTITRIDLALDFFDGEYTPDQ
      |||
a972      VHF GGQRNTVLVELKGTGCSVASPGWELRLKQFLDDSI RTITRIDLALDFFDGEYTPDQ
      130     140     150     160     170     180

      190     200     210     220     230     240
m972.pep ALLDHDNGFFDNSNQRPKSETIGTAWRNE DSGKTFYVGRKKNRFRVRYEKGRQLGDKE
      |||
a972      ALLDHDNGFFDNSNQRPKSETIGTAWRNE DSGKTFYVGRKKNRFRVRYEKGRQLGDKE
      190     200     210     220     230     240

      250     260     270     280     290     300
m972.pep SKWVRFEIQFNYGDIEIPLDILINQGSYFCGAFFICRKFKNMPVPERFDQKKKLNLTFE
      |||
a972      SKWVRFEIQFNYGDIEIPLDILINQGSYFCGAFFICRKFKNMPVPERFDQKKKLNLTFE
      250     260     270     280     290     300
```

1380

	310	320	330	340	350	360
m972.pep	HKLHYAKNAVGLVNFMIEMGFDNSEIVESLKADSGFPKGLEPEKYALEMLRDGLKHGFI					
a972	HKLHYAKNAVGLVNFMIEMGFDNSEIVESLKADSGFPKGLEPEKYALEMLRDGLKHGFI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m972.pep	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPDYDVEKERKQYELSKVYHQNVVDYD					
a972	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPDYDVEKERKQYELSKVYHQNVVDYD					
	370	380	390	400	410	420
m972.pep	YFX					
a972	YFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2949>:

g973.seq

```

1  ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCG
51  actCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA ACAGGAAGTT TTTGATGCCG ACACACTGAC CCGGCTGGAA
151 AAAGTATTGG ACTTTGCCGA GCTGGAAGTG CGCGATGCCA TGATTACGCG
201 CAGCCGCATG AACGTATTGA AAGAAAACGA CAGCATCGAA CGCATCACCG
251 CCTACGTCAT CGATACCGCC CATTGCGGCT TCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTCAACCCC GAGCAGTTCC ACCTGAAATC CGTCTTGCGC CCTGCCGTTT
401 TCGTGCCCGA AGGCAAATCT TTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
501 TTTGGTCACC TTTGAAGACA TCATCGAGCa aatcgctcgtt gacaTCGAAG
551 ACGAGTTTGA CGAAGACGAA AGCGccgacg acatCCAATC cgTTTccgCC
601 GAACGCTGGC GCATCCacgc ggctaCCGAA ATCGAAGaca TCAACGCCTT
651 TTTGCGTACG GAatacggca gcgaagaagc cgacaccatc ggcggttTGG
701 TCATTTCAGGA ATTGGGACAC CTGCCCCGTC GCGGCGAAAA AGTCCCTTAtc
751 ggcgGTTTGC agttcacccgt CGCCCCGCGC GACAACCGCC GCCTGCACAC
801 GCTGATGGCG ACCCGCGTGA AGTAAGCAGA GCCTGCCcgc accgccgttt
851 CTGCacAGTT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2950; ORF 973.ng>:

g973.pep

```

1  MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLROAHEQEV FDADTLTRLR
51  KVLDFAELEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFPN EQPHLKSCLR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGGLV FEDIIEQIVG DIEDEFDEDE SADDIHSVSA
201 ERWRIHAATE IEDINAFFGT EYGSEADTI GGLVIQELGH LPVRGEKVL
251 GGLQFTVARA DNRRHLTLMA TRVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2951>:

m973.seq

```

1  ATGGACGGCG CACAACCGAA AACGAATTTT TTTGAACGCC TGATTGCCCG
51  ACTGCCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA GCAGGAAGTT TTTGATGCCG ATACGCTTTT AAGATTGGAA
151 AAAGTCCTCG ATTTTCCGA TTTGGAAGTG CGCGACGCGA TGATTACGCG
201 CAGCCGTATG AACGTTTAA AAGAAAACGA CAGCATCGAG CGCATCACCG
251 CCTACGTTAT CGATACCGCC CATTGCGGCT TCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTTAACCCC GAGCAGTTCC ACCTCAAATC CATTCTCCGC CCCGCCGTCT
401 TCGTCCCCGA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCGAT TGTCATCGAC GAATACGGCG GCACATCCGG
501 CTTGGTCACC TTTGAAGACA TCATCGAGCA AATCGTCGGC GAAATCGAAG
551 ACGAGTTTGA CGAAGACGAT AGCGCCGACA ATATCCATGC CGTTTCTTCm
601 GaACGcTGGC GCATCCATGC AGTACCGAA ATCGAAGACA TCAACACCTT

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1381

651 CTTCCGGCACG GAATACAGCA kCGAAGAAGC CGACACCATT GGCGGCCTGG
 701 TCATTCAAGA GTTGGGACAT CTGCCCCGTGC GCGGCGAAAA AGTCCTTATC
 751 GGCGGTTTGC AGTTCACCGT CGCACGCGCC GACAACCGCC GCCTGCATAC
 801 GCTGATGGCG ACCCGCGTGA AGTAA

This corresponds to the amino acid sequence <SEQ ID 2952; ORF 973>:

m973.pep

1 MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLRLLE
 51 KVLDFSDLEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
 101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
 151 QRNHMAIVID EYGGTSGGLVT FEDIIEQIVG EIEDEFDEDD SADNIHAVSS
 201 ERWRIHAATE IEDINTFFGT EYSXEEADTI GGLVIQELGH LPVRGEKVLII
 251 GGLQFTVARA DNRRLHTLMA TRVK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 973 shows 95.6% identity over a 274 aa overlap with a predicted ORF (ORF 973.ng) from *N. gonorrhoeae*:

m973/g973

m973.pep	10	20	30	40	50	60
	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLLEKVLDFSDLEV					
g973	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLLEKVLDFAELEV					
	10	20	30	40	50	60
m973.pep	70	80	90	100	110	120
	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
g973	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	70	80	90	100	110	120
m973.pep	130	140	150	160	170	180
	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGGLVTFEDIIEQIVG					
g973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGGLVTFEDIIEQIVG					
	130	140	150	160	170	180
m973.pep	190	200	210	220	230	240
	EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH					
g973	DIEDEFDEDESADDIHSVSAERWRIHAATEIEDINAFGTEYSGEEADTIGGLVIQELGH					
	190	200	210	220	230	240
m973.pep	250	260	270			
	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
g973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2953>:

a973.seq

1 ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCG
 51 ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTGACC CTGTTGCGCC
 101 AAGCGCACGA ACAGGAAGTA TTTGATGCGG ATACGCTTTT AAGATTGGAA
 151 AAAGTCCTCG ATTTTCTCTGA TTTGGAAGTG CCGACGCGA TGATTACGCG
 201 CAGCCGTATG AACGTTTAA AAGAAAACGA CAGCATCGAA CGCATCACCG
 251 CCTACGTTAT CGATACCGCC CATTCGCGCT TCCCCGTCAT CGGTGAAGAC
 301 AAAGACGAAG TTTTGGGTAT TTTGCACGCC AAAGACCTGC TCAAATATAT
 351 GTTCAACCCC GAGCAGTTCC ACCTCAAATC GATATTGCGC CCTGCCGTCT
 401 TCGTCCCCGA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA
 451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
 501 TTTGGTAACT TTTGAAGACA TCATCGAGCA AATCGTCGGC GACATCGAAG
 551 ATGAGTTTGA CGAAGACGAA AGCGCGGACA ACATCCACGC CGTTTCCGCG

1382

```
601 GAACGCTGGC GCATCCACGC GGCTACCGAA ATCGAAGACA TCAACGCCTT
651 TTTCGGCACG GAATACAGCA GCGAAGAAGC CGACACCATC GCGGCGCTGG
701 TCATTACAGGA ATTGGGACAC CTGCCCGTGC GCGGCGAAAA AGTCCTTATC
751 GCGCGTTTGC AGTTCACCGT CGCCCGCGCC GACAACCGCC GCCTGCATAC
801 GCTGATGGCG ACCCGCGTGA AGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2954; ORF 973.a>:

```
a973.pep
1 MDGAQPKTNF FERLIARLAR EPDSAEDVLT LLRQAHEQEV FDADTLLRLE
51 KVLDFSLEVD RDAMITSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMENP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGGLVT FEDIIEQIVG DIEDEFDEDE SADNIHAVSA
201 ERWRIHAATE IEDINAFPGT EYSSEADTI GGLVIQELGH LPVRGEKVL
251 GGLQFTVARA DNRRLHTLMA TRVK*
```

m973/a973 97.8% identity in 274 aa overlap

```

      10      20      30      40      50      60
m973.pep MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLLRLEKVLDFSLEVD
a973      MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLLRLEKVLDFSLEVD
      10      20      30      40      50      60

      70      80      90     100     110     120
m973.pep RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMENP
a973      RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMENP
      70      80      90     100     110     120

      130     140     150     160     170     180
m973.pep EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGGLVTFEDIIEQIVG
a973      EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGGLVTFEDIIEQIVG
      130     140     150     160     170     180

      190     200     210     220     230     240
m973.pep EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH
a973      DIEDEFDEDESADNIHAVSAERWRIHAATEIEDINAFPGTEYSSEEADTIGGLVIQELGH
      190     200     210     220     230     240

      250     260     270
m973.pep LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX
a973      LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX
      250     260     270
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2955>:

```
g981.seq
1 ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCAC TCGCGCTGTC
51 TGCCTGCGGC GGTGAGGCA AGATGCCGC CGCGCTGCC GCGAACCCCG
101 GCAAAGTGTA CCGCGTGGCT TCCAACGCC AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTT GACGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TAAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCCTTGA AACAACGCG ATGCGGACGT TGTGATGTCG
301 GCGGTAACCA TTACCGACGA CCGCAAACAG TCTATGGATT TCAGCGACCC
351 GTATTTTGAA ATCACCAGG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401 CTTCTTCCGA AGATTTGAAA AAGATGAACA AAGTCGGCGT GGTACCGGC
451 CACACGGGCG ATTTCTCCGT TTCCAAACTC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTCGAAAACG TCCCCCTGAT TATCAAGAA CTGGAACACG
551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CGGTATCGC CAATTATGTG
601 AAAACAACC CCGCCAAAGG AATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATCTACG CCAATATTTT TGCCAAAGAG GCGGACAGG CTGCGAAATA
801 A
```

This corresponds to the amino acid sequence <SEQ ID 2956; ORF 981.ng>:

```
g981.pep
1  MKKWIAAALA CSALALSACG GQGKDAAPAA ANPGKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVVMs
101 GVTITDDRQK SMDFSDPYFE ITQVVLVPKG KKVSSSEDLK MNKVGCVVTG
151 HTGDFSFSKL LGNDNPFIAR FENVPLIIKE LENGGLDSV SDSAVIANVY
201 KNNPAKGMDV VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE GGQAAK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2957>:

```
m981.seq
1  ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCGC TCGCGCTGTC
51  TGCCTGCGGC GGTGAGGCA AAGATACCGC CGCGCTGCC GCCAACCCCG
101 ACAAAGTGTG CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAATAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCGCCTTA AACAACGGCG ATGCGGACGT TGTGATGTCG
301 GCGGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGAA ATCACCCTAAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401 CTTCTTCCGA AGATTTGAAA AACATGAACA AAGTCGGCGT GGTAAACGGC
451 TACACGGGCG ATTTCTCCGT ATCCAACTC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTGAAAACG TTCCCCTGAT TATCAAAGAA CTGGAAAACG
551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CGGTCATCGC CAATTATGTG
601 AAAAAAATC CGGCCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATTACG CCAAATATTT TGCAAAAGAA GACGGACAGG CCGCAAAATA
801 A
```

This corresponds to the amino acid sequence <SEQ ID 2958; ORF 981>:

```
m981.pep
1  MKKWIAAALA CSALALSACG GQGKDTAAPA ANPDKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVVMs
101 GVTITDDRQK SMDFSDPYFE ITQVVLVPKG KKVSSSEDLK MNKVGCVVTG
151 YTGDFSFSKL LGNDNPFIAR FENVPLIIKE LENGGLDSV SDSAVIANVY
201 KNNPAKGMDV VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE DGQAAK*
```

m981/g981 98.1% identity in 266 aa overlap

```

      10      20      30      40      50      60
981.pep  MKKWIAAALAC SALALSACGGQGKDTAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF
          |||
g981      MKKWIAAALAC SALALSACGGQGKDAAPAAANPGKVYRVASNAEFAPFESLDSKGNVEGF
          |||
      10      20      30      40      50      60

      70      80      90     100     110     120
981.pep  DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVVMsGVTITDDRQKSMDFSDPYFE
          |||
g981      DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVVMsGVTITDDRQKSMDFSDPYFE
          |||
      70      80      90     100     110     120

      130     140     150     160     170     180
981.pep  ITQVVLVPKGKKVSSSEDLKMNKVGCVVTGYTGDFSFSKLLGNDNPFIARFENVPLIIKE
          |||
g981      ITQVVLVPKGKKVSSSEDLKMNKVGCVVTGHTGDFSFSKLLGNDNPFIARFENVPLIIKE
          |||
      130     140     150     160     170     180

      190     200     210     220     230     240
981.pep  LENGGLDSVSDSAVIANVYKNNPAKGMDVTLPDFTTEHYGIAVRKGDEATVKMLNDAL
          |||
g981      LENGGLDSVSDSAVIANVYKNNPAKGMDVTLPDFTTEHYGIAVRKGDEATVKMLNDAL
          |||
      190     200     210     220     230     240

      250     260
981.pep  EKVRESGEYDKIYAKYFAKEDGQAAKX
          |||
g981      EKVRESGEYDKIYAKYFAKEGGQAAKX
          |||
      250     260
```

```

a981.seq
1  ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCCGCGC TCGCGCTGTC
51  TGCCTGCGGC GGTCAAGGTA AAGATGCCGC CGCGCCCGCC GCAAATCCCG
101 ACAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCGCCTTG AACAACGGCG ATGCGGACGT TGTGATGTCG
301 GGCCTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGA AATCCCAAG TCGTCTCGT TCGGAAGGC AAAAAATAT
401 CTTCTTCCGA AGATTTGAAA AACATGAACA AAGTCGGCGT GGTAACCGCG
451 TACACGGGCG ATTTCTCCGT ATCCAAACTC TTGGGCAACG ACAACCCGAA
501 AATCGCGCGC TTTGAAAACG TTCCCTGAT TATCAAAGAA CTGGAAAACG
551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CAGTCATCGC CAATTATGTG
601 AAAAACAATC CGACCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG AAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAAATCTACG CCAATATTTT TGCAAAAGAA GACGACAGG CCGCAAAATA
801 A

```

This corresponds to the amino acid sequence <SEQ ID 2960; ORF 981.a>:

a981.pap

1	<u>MKKWIAAALA</u>	<u>CSALALSACG</u>	GQGKDAAAPA	ANPDKVYRVA	SNAEFAPFES
51	LDSKGNVEGF	DVDLMNAMAK	AGNFVKIEFKH	QPWDSLFPAI	NNGDADVVMs
101	GVTTIDDRKQ	SMDFSDPYEF	ITQVVLVPGK	KKISSSEDLK	NMNKVGVVTH
151	YTGDFSVSCL	LGNDNPKIAR	FENVPLIIKE	LENGGLDSVV	SDSAVIANYV
201	KNNPTKGMDF	VTLPDFTEH	YGIARVKGDE	ATVTKMLNDAL	KKVRESGEYD
251	KIYAKYFAKE	DGAAAP*			

m981/a981 98.5% identity in 266 aa overlap

		10	20	30	40	50	60
m981.pep		MKKWIAAALACSALALSACGGQGKDTAAPAAPNDKVYRVASNAEFAPFESLDSKGNVEGF					
a981		MKKWIAAALACSALALSACGGQGKDAAPAAPNDKVYRVASNAEFAPFESLDSKGNVEGF					
		10	20	30	40	50	60
		70	80	90	100	110	120
m981.pep		DVDLMNAMAKAGNFKIEFKHPWDSLFPALNNGDADVVMMSGVTITDDRQSMDFSDPYFE					
a981		DVDLMNAMAKAGNFKIEFKHPWDSLFPALNNGDADVVMMSGVTITDDRQSMDFSDPYFE					
		70	80	90	100	110	120
		130	140	150	160	170	180
m981.pep		ITQVVLVPKGKKVSSSEDLKNMNKVGVTGYTGDFSVSKLLGNDNPKIARFENVPLIIKE					
a981		ITQVVLVPKGKKISSSEDLKNMNKVGVTGYTGDFSVSKLLGNDNPKIARFENVPLIIKE					
		130	140	150	160	170	180
		190	200	210	220	230	240
m981.pep		LENGGLDSVVSDSAIVANYVKNNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
a981		LENGGLDSVVSDSAIVANYVKNNPTKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
		190	200	210	220	230	240
		250	260				
m981.pep		EKVRESGEYDKIYAKYFAKEDGQAAKX					
		:					
a981		KKVRESGEYDKIYAKYFAKEDGQAAKX					
		250	260				

1385

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2961>:

```

g982.seq
1   atcgcatcgc aaaaccttcg attcgacaat cgattcctcc aaaaaatggt
51  caacggcgTg aatattttgc cggccgcCga ttgggtagcC ttgGGcgCgCA
101 AAGCCGCAA CGTGGTGGTT GACCGCGCTT TCGGCGGCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TAAAAGAAGT CGCGTCCAAA ACCAAcgaCg
251 tagCCGgcga cggtagcact accgCCACCG TATTGGCACA ATCCATCGTT
301 GCCGAaggcA TGAATACGT TACCGCCGGC ATGAACCCGA CCGATCTGAA
351 ACGCGGCATC GACAAAGccg ttgCCGCTtt ggttgAAGAg cTGAAAAACA
401 TCGCCAAACC TTGCGATACT TCCAAAGAAA TCGCCCAAGT CGGCTCGATT
451 TCCGCCAACT CCGACGAACA AGtcgGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGcg tgattacCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCCCCTTACT TTATCAACGA CGCGGAAAAA CAAATCGCCG GTCTGGACAA
651 TCCGTTTGTT TTGCTGTTCG ACAAAAAAAT CAGCAACATC CGCGACCTGC
701 TGCCCGTGTT GGAACAAGTG GCGAAAGCCA GCCGCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATC CTGAAAACCG TTGCCGTCAA AGCccccggc tTCGGcGACC
851 GCCGCAAAGC GATgctgcaa gaCATCGCCA TCCTGACcgg cggcgTagtG
901 ATTccGAAG Aagtccggcct GTCTTTGGAA AAagcgactT TGgacgaCTT
951 Gggtcaaacc aaACGcatCG AAATCGGtga agaaaacact ACCGTCATcg
1001 acgGCTTCGG CGACGcagcC CAAAtcgaag cgCGTGTTCG CGAAATCCGC
1051 CAACAAATCG AAACCGCGAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AAATGGCAG GAGGCGTGGC AGTGATCAA GTCCGCGCGG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCGCGTGGA AGACCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CGCGCCCGTG CCGCTTTGGA AAACCTGCAC ACCGGAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTAT TGCGCGCCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGA GAACCCAGCG TGGTGGTGAA
1401 CAAAGTGTTG GAAGGCAAAG GCAactacgG TTACAACGCa ggctcCGGCG
1451 AATACGgcga CATGATCGGA ATGGGCGTAC TCGACCCTGC CAAAGTAACC
1501 CGTTCCGCGC TGCAACACGC CGCGTCTatC GCCGGTCTGA TGCTGACGAC
1551 CGACTGCATG ATTGCCGAAA TCCCTGAAGA AAAACCGGCT GTGCCCGATA
1601 TGGGGGGAAT GGGCGGTATG GGCGGCATGA TGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2962; ORF 982.ng>:

```

g982.pep
1   IASQNLRFDN RFLQKMVNGV NILPAADWVA LGAKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGT TATVLAQSIV
101 AEGMKYVTAG MNPTDLKRG I DKAAALVEE LKNIAPCDT SKEIAQVGS I
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KSLNELDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LLFDKKISNI RDLLPVLEQV AKASRPLLI I
251 AEDVEGEALA TLVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGGVV
301 ISEEVGLSLE KATLDDLQGT KRIEIGEENT TVIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALLENLH TGNADQDAGV QIVLRAVESP
451 LRQIVANAGG EPSVVVNKVL EGKGNYGYN A GSGEYGMIG MGVLDPKVT
501 RSALQHAASI AGLMLTTDCM IAEIPEEKPA VPDMGGMGGM GGMM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2963>:

```

m982.seq
1   ATGGCAGCAA AAGACGTACA GTTCGGCAAT GAAGTCCGTC AAAAAATGGT
51  AAACGGCGTG AACATTCTGG CAAACGCCGT CCGCGTAACC TTGGGCCCCA
101 AAGGTCGCAA CGTAGTCGTT GACCGCGCAT TCGGCGGCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TGAAGAAGT TGCGTCCAAA ACCAACGACG
251 TGGCAGGCGA CGGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
301 CCCGAAGGTA TGAATATGT TACCGCAGGT ATGAATCCGA CCGACCTGAA
351 ACGCGGTATC GATAAAGCCG TCGCCGCTTT GGTGACGAA CTGAAAAACA
401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CCGACGAACA AGTCGGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAGTCTTTGG
551 AAAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TGCGGAAAAA CAAATCGCTG CTTTGACAA

```

m982.seq

1	ATGGCAGCAA	AAGACGTACA	GTTCCGCAAT	GAAGTCCGTC	AAAAAATGTT
51	AAACGGCGTG	AACATTCTGG	CAAACGCCGT	CCGCGTAACC	TTGGGCCCCA
101	AAGTGCGBAA	CGTAGTCTGT	GACCGCGCAT	TCGCGGCCCC	GCACATCACC
151	AAAGACGGCG	TAACCGTCGC	CAAGAAATC	GAAGTCAAAG	ACAAGTTTGA
201	AAATATGGGC	GCGCAATATG	TGAAAGAAAT	TGCGTCCAAA	ACCAACGACG
251	TGGCAGGCGA	CGGTACGACT	ACCGCCACCG	TACTGGCGCA	ATCCATCGTT
301	GCCGAAGGTA	TGAAATATGT	TACCGCAGGT	ATGAATCCGA	CCGACCTGAA
351	ACGCGGTATC	GATAAAGCCG	TCGCGCGTTT	GGTTGACGAA	CTGAAAAACA
401	TCGCCAAATC	TTGCGACACT	CTAAAGAAA	TCGCCCAAGT	CGGCTCTATT
451	TCCGCCAACT	CCGCGCAACA	AGTCGGCGCG	ATTATCGCGC	AAGCGATGGA
501	AAAAGTCGGC	AAAGAAGGCG	TGATTACCGT	TGAAGACGGC	AAGTCTTTGG
551	AAAACGAGCT	GGACGTAGTT	GAAGGTATGC	AGTTCGACCG	CGGCTACCTG
601	TCTCCTTACT	TCATCAACGA	TGCGGAAAAA	CAAATCGCTG	CTTTGGACAA
651	TCGCTTTGTA	TGTTGTGTCG	ACAAAAAATC	CAGCAACATC	CGGACCTTGC
701	TGCCTGTTTT	GGAACAAGTG	GCAAAAGCCA	GCCGTCGCGT	CTTGATTATG
751	GCTGAAGACG	TAGAAGGCGA	AGCCTTGCGC	ACTTTGGTCG	TGAACAACAT
801	CCGAGGCATC	CTGAAAACCG	TTGCCGTCAA	AGCCCCGGGC	TTCCGGCGACC
851	CGCGCAAGC	GATGTTGCAA	GACATCGCCA	TCCTGACCCG	CGGCGTGGTG
901	ATTTCCGAAG	AGTCCGCTCT	GTCTTTGGAA	AAAGCGACTT	TGGACGACTT
951	GGGTCAAGCC	AAACGCATCG	AAATCGGTAA	AGAAAACACC	ACCATCATTC
1001	ACGGCTTTTG	CGACGCAGCC	CAAATCGAAG	CGCGTGTTCG	CGAAATCCGC
1051	CAACAAATCG	AAACCGCAAC	CAGCGATTAC	GACAAAGAAA	AACTGCAAGA
1101	GCGCGTGGCT	AATTTGGCAG	CGGGCGTGCC	AGTCATCAAA	GTCCGTTGCCG
1151	CGACCGAAGT	CGAAATGAAA	GAGAAAAAAG	ACCGCTTGGA	AGACGCGCTG
1201	CACGCTACCC	GCGCAGCCGT	TGAAGAAGGC	GTGGTTGCAG	GCGGCGGCGT
1251	AGCCCTGTTG	CGTGCCCGTG	CTGCTTTGGA	AAACCTGCAC	ACCGGCAATG
1301	CGCACCAGA	CGCAGGCGTA	CAAACTCGTCT	TGCGCGCCGT	TGAGTCTCCG
1351	CTGCGCCAAA	TCGTTGCCAA	CGCAGGCGCG	GAAACCAGCG	TGGTGTGTAA
1401	CAAAGTATTG	GAAGGCAAAAG	GCAACTACGG	TTACAACGCT	GGGACGCGCG
1451	AATACGCGCA	TATGATCGAA	ATGGGCGTAC	TCGACCCCGC	CAAAGTAACC
1501	CGTTCTGCGC	TGCAACACGC	CGCATCTATC	GCCGCGCTTG	TGCTGACCAC
1551	TGATTGCATG	ATCGCTGAAA	TCCCGGAAGA	CAACCCGGCT	GTGCTGATA
1601	TGGGCGGCAT	GGGTGGTATG	GGCGGCATGA	TGTAA	

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from *N. gonorrhoeae*

m982/g982 95.8% identity in 544 aa overlap

```
m982.pep      MAAKDVFQGNEVRQKMGVGNILANAVRVTLGPKGRNVVDRAFGGPHTITKDGVTVAKEI
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1387

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g982      IASQNLRFDNRFLOKMNNGVNILPAADWVALGAKGRNVVVDRAFGGPHITKDGVTVAKEI
           10      20      30      40      50      60

           70      80      90      100     110     120
m982.pep  ELKDKFENMGAQMVKEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPDLKRG
           |||||
g982      ELKDKFENMGAQMVKEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPDLKRG
           70      80      90      100     110     120

           130     140     150     160     170     180
m982.pep  DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
           |||||:|||||
g982      DKAVAALVEELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
           130     140     150     160     170     180

           190     200     210     220     230     240
m982.pep  KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
           |||||:|||||
g982      KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
           190     200     210     220     230     240

           250     260     270     280     290     300
m982.pep  AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGVV
           |||||
g982      AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGVV
           250     260     270     280     290     300

           310     320     330     340     350     360
m982.pep  ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY
           |||||:|||||
g982      ISEEVGLSLEKATLDDLQAKRIEIGEENTTVIDGFGDAAQIEARVAEIRQQIETATSDY
           310     320     330     340     350     360

           370     380     390     400     410     420
m982.pep  DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL
           |||||
g982      DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL
           370     380     390     400     410     420

           430     440     450     460     470     480
m982.pep  RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNVKVLGKGNYGNA
           |||||
g982      RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNVKVLGKGNYGNA
           430     440     450     460     470     480

           490     500     510     520     530     540
m982.pep  GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGGM
           |||||
g982      GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEEKPAVPDMGGMGGM
           490     500     510     520     530     540

m982.pep  GMMMX
           |||||
g982      GMMMX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2965>:

```

a982.seq
1   ATGGCAGCAA AAGACGTACA ATTCGGCAAT GAAGTCCGCC AAAAAATGGT
51  AAACGGCGTG AACATTTTGG CAAACGCCGT GCGCGTAACC TTGGGTCCCA
101 AAGGCCGCAA CGTGGTGGTT GACCGCGCTT TCGGCGGCCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TGAAAGAAGT CGCGTCCAAA ACCAACGACG
251 TGGCGGGCGA CGGTACGACT ACCGCCACCG TATTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAAATACGT TACCGCCGGT ATGAACCCGA CCGACCTGAA
351 ACGCGGTATC GACAAAGCCG TCGCCGCTTT GGTGAAGAG CTGAAAAACA

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1388

```
401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CTGACGAACA AGTCGGCGCG ATTATTGCGG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AATTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TCGCGAAAAA CAAATCGCCG GCTTGACAA
651 TCCGTTTGTA TTGCTGTTTC AAAAAAAAT CAGCAATATC CGCGACCTGC
701 TGCCTGTTTT GGAACAAGTG GCCAAAGCCA GCCGTCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATT CTGAAAACCG TTGCCGTTAA AGCTCCGGGC TTCGGCGACC
851 GCCGCAAAGC GATGCTGCAA GACATCGCTA TCCTGACCGG CGGCACAGTG
901 ATTTCCGAAG AAGTCGGCCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951 GGGTCAGGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1001 ACGGCTTCGG CGACGCAGCC CAAATCGAAG CGCGTGTGCG CGAAATCCGC
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AAACCTGGCAG GCGGCGTGGC AGTAATCAAA GTCGGTGCCG
1151 CGACCGAAGT GGAAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CCGCCCCGTG CCGCTCTGGA AAACCTGCAC ACCGGCAATG
1301 CAGACCAAGA CGCAGGCGTA CAAATCGTCT TGCGCGCCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1401 CAAAGTGTG GAAGGCAAAG GCAACTATGG TTACAACGCT GGCAGCGGCG
1451 AATACGCCGA CATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501 CGTTCGCGC TGCAACACGC CGCGTCTATC GCCGGCCTGA TGCTGACCAC
1551 AGACTGCATG ATTGCTGAAA TCCCTGAAGA CAAACCGGCT ATGCCTGATA
1601 TGGGCGGCAT GGGTGGTATG GCGGCATGA TGTA
```

This corresponds to the amino acid sequence <SEQ ID 2966; ORF 982.a>:

a982.pep

```
1 MAAKDVQFGN EVRQKMVNGV NILANAVRVT LGPKGRNVVV DRAFGGPHIT
51 KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGT TATVLAQSIV
101 AEGMKYVTAG MNPTDLKRG DKAVAALVEE LKNIKPCDT SKEIAQVGS
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KLENELDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LLFDKKISNI RDLLPVLEQV AKASRPLLI
251 AEDVEGEALA TLVNNIRGI LKTVAVKAPG FGDRRKAMLO DIAILTGGTV
301 ISEEVGLSLE KATLDDLQGA KRIEIGKENT TIIDGFGDAA QIEARVAEIR
351 QIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALLENH TGNADQDAGV QIVLRAVES
451 LRQIVANAGG EPSVVVNKVL EGKGNYGNA GSGEYGMIE MGVLDPKAVT
501 RSALQHAASI AGLMLTTDCM IAEIPEDKPA MPDMGGMGGM GGMM*
```

m982/a982 99.3% identity in 544 aa overlap

```
10 20 30 40 50 60
m982.pep MAAKDVQFGNEVRQKMVNGVNILANAVRVTLGPKGRNVVV DRAFGGPHITKDGVTVAKEI
|||||
a982 MAAKDVQFGNEVRQKMVNGVNILANAVRVTLGPKGRNVVV DRAFGGPHITKDGVTVAKEI
10 20 30 40 50 60

70 80 90 100 110 120
m982.pep ELKDKFENMGAQMVKEVASKTNDVAGDGT TATVLAQSIVAEGMKYVTAGMNPTDLKRG
|||||
a982 ELKDKFENMGAQMVKEVASKTNDVAGDGT TATVLAQSIVAEGMKYVTAGMNPTDLKRG
70 80 90 100 110 120

130 140 150 160 170 180
m982.pep DKAVAALVDELKNIKPCDTSKEIAQVGSISANSDEQVGAI IAEAMEKVGKEGVITVEDG
|||||:|||||
a982 DKAVAALVEELKNIKPCDTSKEIAQVGSISANSDEQVGAI IAEAMEKVGKEGVITVEDG
130 140 150 160 170 180

190 200 210 220 230 240
m982.pep KLENELDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
|||||:|||||
a982 KLENELDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
190 200 210 220 230 240
```

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	250	260	270	280	290	300
m982.pep	AKASRPLLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGVV					
a982	AKASRPLLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m982.pep	ISEEVGLSLEKATLDDLGOAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY					
a982	ISEEVGLSLEKATLDDLGOAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY					
	310	320	330	340	350	360
	370	380	390	400	410	420
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
a982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
	370	380	390	400	410	420
	430	440	450	460	470	480
m982.pep	RARAALNLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNKVLEGKNGYGYNA					
a982	RARAALNLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNKVLEGKNGYGYNA					
	430	440	450	460	470	480
	490	500	510	520	530	540
m982.pep	GSGEYGDMIEMGVLDPKAVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGM					
a982	GSGEYGDMIEMGVLDPKAVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGM					
	490	500	510	520	530	540
m982.pep	GGMMX					
a982	GGMMX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2967>:

g986.seq

1	GTGTTCAAAA	AATACCAATA	CTTCGCTTTG	GCGGCACTGT	GTGCCGCTTT
51	GCTGGCAGGC	TGCGAAAAGG	CAGGCAGCTT	TTTCGGTGCG	GACAAAAAAG
101	AAGCATCCTT	CGTAGAACGC	ATCGAACACA	CCAAAGACGA	CGGCAGTGTC
151	AGTATGCTGC	TGCCCCGACTT	TGCCCAACTG	GTTCAAAGCG	AAGGCCCGGC
201	AGTCGTCAAT	ATTCAGGCAG	CCCCCGCCCC	GCGCACCCAA	AACGGCAGCG
251	GCAATGCCGA	AACCGATTCC	GACCCGCTTG	CCGACAGCGA	CCCGTTCTAC
301	GAATTTTCA	AACGCCTCGT	CCCGAACATG	CCCGAAATCC	CCCAAGAAGA
351	AGCAGATGAC	GGCGGATTGA	ACTTCGGTTC	GGGCTTCATC	ATCAGCAAAA
401	ACGGCTACAT	CCTGACCAAT	ACCCACGTCG	TTGCCGGTAT	GGGCAGTATC
451	AAAGTCCTGC	TCAACGACAA	GCGCGAATAT	ACCGCCAAAC	TCATCGGTTC
501	GGATGTCCAA	TCCGATGTCG	CCCTTCTGAA	AATCGACGCA	ACGGAAGAGC
551	TACCCGTCGT	CAAAATCGGC	AATCCCAAAA	ATTGAAACC	GGGCGAATGG
601	GTCGCTGCCA	TCGGCGCGCC	CTTCGGCTTT	GACAACAGCG	TGACCGCCGG
651	CATCGTGTCC	GCCAAAGGCA	GAAGCCTGCC	CAACGAAAgc	tACACACCCT
701	TCATCCAAAC	CGACGTTGCC	ATCAATCCGG	GCAATTCCGG	CGGCCCGCTG
751	TTCAACTTAA	AAGGACAGGt	cgTCGGCATC	AATTCGCAAA	TATACAGCCG
801	CAGCGgcgga	ttCATGGGCA	TCTCCTTTGC	CATCCCGATT	GACGTTGCCA
851	TGAATGTCGC	CGAACAGCTG	AAAAACACCG	GCAAAGTCCA	ACGCGGACAA
901	CTGGGCGTGA	TTATTTCAGGA	AGTATCCTAC	GGTTTGCCAC	AGTCGTTCCG
951	TCTGGATAAA	GCCAGCGGCG	CATTGATTGC	CAAAATCCTT	CCCGGCGAGCC
1001	CCGAGAACG	TGCCGGCCTG	CAGGCGGGCG	ACATCGTCTT	CAGCCTCGAC
1051	GGCGGAGAAA	TACGTTCTTC	CGGCGACCTT	CCCGTCATGG	TCGGCGCCAT
1101	TACGCCGGA	AAAGAAGTCA	GCCTCGGCGT	ATGGCGCAAA	GGCGAAGAAA
1151	TCACAATCAA	AGCCAAGCTG	GGCAACGCCg	ccgagcATAC	CGGCgcacCA
1201	TCCAAAACAG	ATGAAgcccc	ctacaccgAA	CAGCAATCCG	GTACGTTCTC
1251	GGTCGAATCC	GCAGGCATTA	CCCTTCAGAC	ACATACCGAC	AGCAGCGGca
1301	aacacctcgt	cgtcgtacg	gtttccgacg	cggcagaacg	cGCAGGCTTA

1390

1351 AGgcgcggcg acgaaatcct cgcgggtcggg caagtccccg tcaatgacga
 1401 agccgGTTTC cgcaaaGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
 1451 TGGTCatgcg ccgTGGCAAC ACGCTGTTCA TCGCATTAAA CCTGCAATAA

This corresponds to the amino acid sequence <SEQ ID 2968; ORF 986.ng>:

g986.pep

1 VFKKYQYFAL AALCAALLAG CEKAGSFFGA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPVAVN IQAAPAPRTQ NGSGNAETDS DPLADSDPFY
 101 EFFKRLVPNM PEIPQEEADD GGLNFGSGFI ISKNYIILTN THVVAGMGSI
 151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKNLKPGEW
 201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
 251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGO
 301 LGVIIQEVSY GLAQSFGLDK ASGALIAKIL PGSPAERAGL QAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKAKL GNAAEHTGAS
 401 SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGKHLVVVR VSDAAERAGL
 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLVMRRGN TLFIALNLQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2969>:

m986.seq

1 GTGTTCAAAA AATACCAATA CCTCGCTTTG GCAGCACTGT GTGCAGCCTC
 51 GCTGGCAGGC TGCAGACAAG CAGGCAGCTT CTTCTGTGGCG GACAAAAAAG
 101 AAGCATCCTT CGTAGAACGC ATCGAACACA CCAAAGACGA CGGCAGCGTC
 151 AGTATGCTGC TGCCCGACTT TGCCCAACTG GTTCAAAGTG AAGGTCGGGC
 201 AGTCGTCAAT ATTCAGGCAG CCCCCGCCCC GCGCACCCAA AACGGCAGCG
 251 GCAATGCCGA AACGATTCC GACCCGATTG CCGACAACGA CCCGTTCTAC
 301 GAATTTTTCA AACGCCTCGT CCCGAATATG CCCGAAATCC CCCAAGAAGA
 351 AGCAGATGAC GCGCGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
 401 ACGGCTACAT CCTGACCAAT ACCCACGTCG TTACCGGCAT GGGCAGTATC
 451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTC
 501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
 551 TGCCCGTCGT CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
 601 GTCGCGGCCA TCGGCGCGCC CTTGGGCTTC GACAACAGCG TGACCGCCGG
 651 CATCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCCT
 701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
 751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAAA TATACAGCCG
 801 CAGCGGCGGA TTCATGGGCA TTCTCTTCGC CATCCCGATT GACGTGCCA
 851 TGAATGTCGC CGAACAGCTG AAAAACACCG GCAAAGTCCA ACGCGGACAA
 901 CTGGGCGTGA TTATTCAAGA AGTATCTAC GGTTTGGCAC AATCGTTCGG
 951 TTTGGACAAA GCCGGCGGCG CACTGATTGC CAAAATCCTG CCCGGCAGCC
 1001 CCGCAGAACG TGCCGGCCTG CAGGCGGGCG ACATCGTCTT CAGCTCGAC
 1051 GCGGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
 1101 TACGCCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAAA GGCGAAGAAA
 1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
 1201 TCCAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
 1251 GGTCGAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
 1301 GACACCTCGT CGTCGTACGG GTTTCGACG CGGCAGAACG CGCAGGCTTG
 1351 AGGCGCGGCG ACGAAATTCT TGCCGTTCGG CAAGTCCCCG TCAATGACGA
 1401 AGCCGGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
 1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAAA CCTGCAATAA

This corresponds to the amino acid sequence <SEQ ID 2970; ORF 986>:

m986.pep..

1 VFKKYQYLAL AALCAASLAG CDKAGSFFVA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPVAVN IQAAPAPRTQ NGSGNAENDS DPIADNDPFY
 101 EFFKRLVPNM PEIPQEEADD GGLNFGSGFI ISKDGYILTN THVVVTGMGSI
 151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
 201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
 251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGO
 301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL QAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
 401 SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGHLLVVVR VSDAAERAGL
 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m986/g986 97.0% identity in 499 aa overlap

	10	20	30	40	50	60
m986.pep	VFKKYQYLALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
	:					
g986	VFKKYQYFALAALCAALLAGCEKAGSFFGADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m986.pep	VQSEGPVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPNMPEIPQEEADD					
	:					
g986	VQSEGPVVNIQAAPAPRTQNGSGNAETDSDPLADSDPFYEFFKRLVPNMPEIPQEEADD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m986.pep	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	:					
g986	GGLNFGSGFIISKNGYILTNTHVVAGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m986.pep	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
	:					
g986	TEELPVVKIGNPKNLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m986.pep	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	:					
g986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m986.pep	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
g986	LGVIIQEVSYGLAQSFGLDKASGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m986.pep	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
g986	PVMVGAITPGKEVSLGVWRKGEEITIKAKLGNAAEHTGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
	430	440	450	460	470	480
m986.pep	AGITLQTHTDSSGGHLVVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
g986	AGITLQTHTDSSGKHLVVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
	430	440	450	460	470	480
	490	500				
m986.pep	VPLLIMRRGNTLFIALNLQX					
g986	VPLLVMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2971>:

```

a986.seq
1   GTGTTCAAAA AATACCAATA CCTCGCTTGT GCAGCACTGT GTGCCGCCTC
51  GCTGGCAGGC TGCACAAAG CCGGCAGCTT TTTCGGTGCG GACAAAAAAG
101 AAGCATCCTT TGTAAGACGC ATCAAACACA CCAAAGACGA CGGCAGCGTC
151 AGTATGCTGC TGCCCGACTT TGTCCAACGT GTTCAAAGCG AAGGCCCGGC
201 AGTCGTCAAT ATTCAGGCAG CCCCCGCCCC GCGCACCCAA AACGGCAGCA
251 GCAATGCCGA AACCGATTCC GACCCGCTTG CCGACAGCGA CCCGTTCTAC
301 GAATTTTTC AACGCCTCGT CCCGAACATG CCCGAAATCC CCCAAGAAGA
351 AGCAGATGAC GNGGGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
401 ACGGCTATAT TCTGACCAAT ACGCACGTCTG TTACCGGCAT GGGCAGTATC
451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTC
501 GGATGTCCAA TCCGATGTCTG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TGCCCGTCGT CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
601 GTCGCCGCCA TCGGCGCGCC CTTCGGCTTC GACAACAGCG TGACCGCCGG
651 CNTCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCTT
701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCGCTG
751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAAA TATACAGCCG
801 CAGCGGCGGA TTCATGGGCA TTTCCTTCGC CATCCCGATT GACGTTGCCA
851 TGAATGTCTG CGAACAGCTG AAAAACACCG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTGTGGCAC AATCGTTCGG
951 TTTGGACAAA GCCGGCGGGC CACTGATTGC CAAATCCTG CCCGCGAGCC
1001 CCGCAGAACG TGCCGGCCTG CGGGCGGGCG ACATCGTCTT CAGCCTCGAC
1051 GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
1101 TACGCCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAAA GGCGAAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
1251 GGTCGAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
1301 GACACCTCGT CGTCGTACGG GTTCCGACG CGGCAGAACG CGCAGGCTTG
1351 AGGCGCGGCG ACGAAATTCT TGCCGTGCGG CAAGTCCCCG TCAATGACGA
1401 AGCCGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAAA CCTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2972; ORF 986.a>:

```

a986.pep
1   VFKKYQYLAL AALCAASLAG CDKAGSFFGA DKKEASFVER IKHTKDDGSV
51  SMLLPDFVQL VQSEGPVVN IQAAPAPRTQ NGSSNAETDS DPLADSDPFY
101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKDGYILTN THVVTGMGSI
151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
201 VAAIGAPFGF DNSVTAGXVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIFI DVAMNVAEQL KNTGKVQRGO

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301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL RAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
 401 SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGGHLVVVR VSDAAERAGL
 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

m986/a986 98.2% identity in 499 aa overlap

m986.pep	10	20	30	40	50	60
	VFKKYQYLALAALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
a986	VFKKYQYLALAALCAASLAGCDKAGSFFGADKKEASFVERIKHTKDDGSVSMLLPDFVQL					
	10	20	30	40	50	60
m986.pep	70	80	90	100	110	120
	VQSEGPAVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVFNMPPEIPQEEADD					
a986	VQSEGPAVVNIQAAPAPRTQNGSSNAETDSPLADSDPFYEFFKRLVFNMPPEIPQEEADD					
	70	80	90	100	110	120
m986.pep	130	140	150	160	170	180
	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
a986	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
m986.pep	190	200	210	220	230	240
	TEELPVVKIGNPKDLKPGEWVAAIGAPFGDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
a986	TEELPVVKIGNPKDLKPGEWVAAIGAPFGDNSVTAGXVSAKGRSLPNESYTPFIQTDVA					
	190	200	210	220	230	240
m986.pep	250	260	270	280	290	300
	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQKNTGKVQRGQ					
a986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQKNTGKVQRGQ					
	250	260	270	280	290	300
m986.pep	310	320	330	340	350	360
	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
a986	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLRAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
m986.pep	370	380	390	400	410	420
	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
a986	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
m986.pep	430	440	450	460	470	480
	AGITLQTHTDSSGGHLVVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
a986	AGITLQTHTDSSGGHLVVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
	430	440	450	460	470	480
m986.pep	490	500				
	VPLLIMRRGNTLFIALNLQX					
a986	VPLLIMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2973>:

g987.seq

1 ATGAAAACAC GCAGCCTCAT TTCCCTTTTA TGCCTCCTTC TCTGTTTCATG

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51  TTCTTCATGG TTGCCCCCAC TGGAAGAACG GACGGAAAGC CGTCATTTTA
101  ATACTTCCAA ACCTGTCCCTC CTGGACAACA TCCTGCAAAT CCGGCACACC
151  CCTCATAACA ACGGGCTATC CGACATCTAC CTGCTCGACG ACCCCCACGA
201  AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251  ATTTGCAATA CTACATTTGG CGCAACGaCA TTTCCGGCAG GCTGCTGTTT
301  AACCTCATGT ACCTTGCCGC agaacgcGGC GTGCGCGTAC GCCTGCTGTt
351  ggacgacaAC AACAcgcgcg gcttggacga tctctGCTC GCCCTCGACA
401  GCCATCCCAA TAtctaagtG CGCCTGTTCA ACCCCTTcgt CCTACGCAAA
451  TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCgcCTCA ACCGCCGCAT
501  GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551  GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601  GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651  CTTGACCCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701  TCCGCAGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751  GAAACATCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801  GCCCCTCTAC CAAAAAATAC AGACGGGACG CATCGACTGG CAGAGCGTCC
851  AAACCCGCCT GATCAGCGAC AGCCCTGCAA AAGGACTCGA CCGCGACCGC
901  CGCAAACCGC CGATTGCCGG GAGGCTGCAA GACGCGCTCA AACAGCCCCGA
951  AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCTACA AAATCCGGCA
1001 CAGACGCACT GGCAAAACTG GTGCAGGACG GCATAGACGT TACCGTCTTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTACGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCACAACA TGCCGTCCCC GCCACAAAAG ACAAGGCCCT GACCGGCAGC
1201 TCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGacg gCAAACGCAT
1251 CTTCATCGGC TCATTCAACC TCGACCCCGG TTCCGCACGG CTCAATACCG
1301 AAATGGGCGT CGTCATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 AccctCGCCG AtacCACACC CGAATACGCC TACCGCGTTA CCCTCGACAA
1401 ACACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TCGAAGGTTT ATTATAG

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This corresponds to the amino acid sequence <SEQ ID 2974; ORF 987.ng>:

g987.pep

```

1  MKTRSLISLL CLLCSCSSW LPPLEERTES RHFNTSKPVL LDNILOIRHT
51  PHNGLSDIY LLDDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLMYLAERG VRVRLLLDDN NTRGLDLLLL ALDSHPNI*V RLFNPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD SPAKGLDRDR
301 RKPPIAGRLQ DALKEPEKSV YLVSPYFVPT KSGTDALAKL VQDGDIVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKLGTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVIE SPKIAEQMER
451 TLADTTPEYA YRVTLDKHNR LQWHPATRK TYPNEPEAKL WKRIAANKILS
501 LLPIEGL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2975>:

m987.seq

```

1  ATGAAACAC GCAGCCTAAT TTCCCTTTTA TGCTCCTTC TCTGTTTCATG
51  TTCTTCATGG TTGCCCCCAC TGGAAGAACG GACGGAAAGC CGTCATTTCA
101  ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151  CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCCACGA
201  AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251  ATTTGCAATA CTACATCTGG CGCAACGACA TTTCCGGCAG GCTGCTGTTT
301  AACCTCGTGT ACCTTGCCGC AGAACCGGGT GTGCGCGTAC GCCTGCTGTT
351  GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTT GCCCTCGACA
401  GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451  TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCgcCTCA ACCGCCGCAT
501  GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551  GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTTCGCC
601  GATTTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651  CTTGACCCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701  TCCGCAGCGG CGACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751  GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801  GCCCCTCTAC CAAAAAATAC AGACAGGATG CATCGACTGG CAGAGCGTCC
851  GAACCCGCCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC

```


1395

```

901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCCCA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTTCCACACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTTCTG
1051 ACCAACTCGC TGCAGGCGAC CGACGTTGCC GCGGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAACCTC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCC GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCACGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTTCATCGGT TCGTTCAACC TCGACCCCCG TTCCGCGCGT CTCAACACCG
1301 AAATGGGCGT TGTTCATCGA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCACACC CGCCTACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCC TAGAAGGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2976; ORF 987>:

```

m987.pep
1 MKTRSLISLL CLLCSCSSW LPPLEERTES RHFNTSKPVR LDNILQIRHT
51 PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAERG VRVRLLEDN NTRGLDILL ALDSHPNIEV RLFNPFVLRK
151 WRALGYLTD PRLNRRMHNK SFTADNRAT LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGDIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGCIDW QSVRTRLISD DPAKGLDRDR
301 RKPPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
451 TLADTTPAYA YRVTLDRHNR LQWHDPATRK TYPNEPEAKL WKRIA AKILS
501 LLPIEGLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```

m987/g987 97.8% identity in 508 aa overlap

      10      20      30      40      50      60
m987.pep MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY
          |||
g987      MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVLLDILQIRHTPHNGLSDIY
          |||

      10      20      30      40      50      60
m987.pep LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLEDN
          ||:|||||
g987      LLDDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMLYLAERGVRVRLLEDN
          ||:|||||

      70      80      90      100     110     120
m987.pep LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLEDN
          ||:|||||
g987      LLDDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMLYLAERGVRVRLLEDN
          ||:|||||

      70      80      90      100     110     120
m987.pep LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLEDN
          ||:|||||
g987      LLDDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMLYLAERGVRVRLLEDN
          ||:|||||

      130     140     150     160     170     180
m987.pep NTRGLDILLALDSHPNIEVRLFNPFVLRKWRALGYLTDFFRLNRRMHNKSFTADNRATI
          |||
g987      NTRGLDILLALDSHPNIXVRLFNPFVLRKWRALGYLTDFFRLNRRMHNKSFTADNRATI
          |||

      130     140     150     160     170     180
m987.pep NTRGLDILLALDSHPNIEVRLFNPFVLRKWRALGYLTDFFRLNRRMHNKSFTADNRATI
          |||
g987      NTRGLDILLALDSHPNIXVRLFNPFVLRKWRALGYLTDFFRLNRRMHNKSFTADNRATI
          |||

      190     200     210     220     230     240
m987.pep LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGDIG
          |||
g987      LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIG
          |||

      190     200     210     220     230     240
m987.pep LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGDIG
          |||
g987      LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIG
          |||

      250     260     270     280     290     300
m987.pep KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVRTRLISDDPAKGLDRDR
          |||
g987      KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDSPA KGLDRDR
          |||

      250     260     270     280     290     300
m987.pep KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVRTRLISDDPAKGLDRDR
          |||
g987      KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDSPA KGLDRDR
          |||

      310     320     330     340     350     360
m987.pep RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVL TNSLQATDVA

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1396

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g987      |||||
          RKPP|IAGRLQDALKQPEKSV|YLVSPYFVPTKSGT|DALAKLVQDGIDVTLV|TNSLQATDVA
          310      320      330      340      350      360

          370      380      390      400      410      420
m987.pep  AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS|LHAKTFIVDGKR|FIG
          |||||
g987      AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS|LHAKTFIVDGKR|FIG
          370      380      390      400      410      420

          430      440      450      460      470      480
m987.pep  SFNLDPRSARLNT|EMGVVIESPKIAEQMERT|LADTT|PAYAYRV|TLDRHNR|LQWHP|PATRK
          |||||
g987      SFNLDPRSARLNT|EMGVVIESPKIAEQMERT|LADTT|PEYAYRV|TLDKHNR|LQWHP|PATRK
          430      440      450      460      470      480

          490      500      509
m987.pep  TYPNEPEAKLWKRIA|AAKILSLLPIEGLLX
          |||||
g987      TYPNEPEAKLWKRIA|AAKILSLLPIEGLLX
          490      500

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2977>:

```

a987.seq
1   ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTTCATG
51  TTCTTCATGG TTGCCCCCAC TGGAAGAACG GACGGAAAGC CGTCATTTTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTTCCGGCCG ACTGCTGTTT
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTC GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCCTCA ACCGCCGAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTCGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACAGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCCACA AAATCCGGCA
1001 CAGAGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTCCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCTACCA TGCCGTCCCT GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTCATCGGC TCATTCAACC TCGACCCCGT TTCCGCACGG CTCAATACTG
1301 AAATGGGCGT TGTTATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCTCACC CGAATACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAA AATCCTATCC
1501 CTGCTGCCCA TAGAAAGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 550; ORF 2978.a>:

```

a987.pep
1   MKTRSLISLL CLLLCSCSSW LPPLEERTES RHFNTSKPVR LDNILQIRHT
51  PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAAERG VRVRLLLDDN NTRGLDLLLL ALDShPNIEV RLFNPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD DPAKGLDRDR
301 RKPP|IAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL

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1397

351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
 401 SVTSLHAKTF IVDGKRIFIG SFNLDPARSAR LNTEMGVVIE SPKIAEQMER
 451 TLADTSPEYA YRVTLDNRNR LQWHDPATRK TYPNEPEAKL WKRIAAILLS
 501 LLPIESLL*

m987/a987 98.8% identity in 508 aa overlap

m987.pep	10	20	30	40	50	60
	MKTRSLISLLCLLLCSCSSWLPPEERTESRHFNTSKPVRLDNIQIRHTPHTNGLSDIY					
a987	MKTRSLISLLCLLLCSCSSWLPPEERTESRHFNTSKPVRLDNIQIRHTPHTNGLSDIY					
	10	20	30	40	50	60
m987.pep	70	80	90	100	110	120
	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLLDDN					
a987	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLLDDN					
	70	80	90	100	110	120
m987.pep	130	140	150	160	170	180
	NTRGLDDLLLALDHPNIEVRLFPFVLKWRALGYLTDFFRLNRRMHNKSFTADNRATI					
a987	NTRGLDDLLLALDHPNIEVRLFPFVLKWRALGYLTDFFRLNRRMHNKSFTADNRATI					
	130	140	150	160	170	180
m987.pep	190	200	210	220	230	240
	LGGRNIGDEYFKVGEDTVFADLDILATGSSVVGESHDFRYWASHSAHNATRIIRSGDIG					
a987	LGGRNIGDEYFKVGEDTVFADLDILATGSSVVGESHDFRYWASHSAHNATRIIRSGNIG					
	190	200	210	220	230	240
m987.pep	250	260	270	280	290	300
	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVTRRLISDDPAKGLDRDR					
a987	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRRLISDDPAKGLDRDR					
	250	260	270	280	290	300
m987.pep	310	320	330	340	350	360
	RKPPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLNTSLQATDVA					
a987	RKPPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLNTSLQATDVA					
	310	320	330	340	350	360
m987.pep	370	380	390	400	410	420
	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
a987	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
	370	380	390	400	410	420
m987.pep	430	440	450	460	470	480
	SFNLDPARSARLNTEMGVVIESPKIAEQMERTLADTTPAYAYRVTLDNRNRLQWHDPATRK					
a987	SFNLDPARSARLNTEMGVVIESPKIAEQMERTLADTSPEYAYRVTLDNRNRLQWHDPATRK					
	430	440	450	460	470	480
m987.pep	490	500	509			
	TYPNEPEAKLWKRIAAILLSLLPIEGLLX					
a987	TYPNEPEAKLWKRIAAILLSLLPIESLLX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2979>:

g988.seq

1 ATGAATAAAA ATATTAAATC TTAAATTTA CGGGAAAAAG ACCCGTTTTT

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51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCAGT CGGgaATGGA
101 TAATCGAATT GTTGGAGCGC AAAGGTGTGC CTTCAAAAAT CGAATCGCTT
151 GCACGCGAGC TGTGATTAC GGAAGacgag tATGTCTTTT TTGAACGCCG
201 TCTGAaggCG atgGCGCGGG AcggtCAGGT TTTAATCAAC CGCCgaggcg
251 CagtTTGCGc gGCggacaag ctgGATTTGG TCAAATGccg Cgtcggagcg
301 catAAGGAcg gtttcggett cgcCGTGCCG CTCATGCCGA TGGACGAAGG
351 GGATTTCTGT TTATACGAAC GCCAgatgcg tggTgtcatG CAcggcgaca
401 ccggttACCGT CCGTCTGCGc ggtatggaCC GCAGGGGccg ccgcGAaggg
451 acgtttctGG ATATTGTCGA ACGCGCGCAA AGCAAAGTTG TCGGCCGTTT
501 CTATATGGAT AGGGGCGTGG CGATTTTGGG GCCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTGTGGAA CCGGACGGCG TGGCGCGTTT CAAACCCGAA
601 TCCGGTCAGG TTATCGTCGG CAAAATTGAG GTTTATCCCG AGCAAAACCG
651 GCCTGCAGTG GCAAAAATCA TTGAAGTTT GGGCGATTAT GCCGACAGCG
701 GGATGGAAAt cgAAATTGCC GTGCGCAAGC ATCATTTGCC GCaccgaTTC
751 AGTGAagcgt gtGcCAAATC CGcgaAAAAA Attcccgacc ATGTACGCAA
801 AAGCGATTTG AAAGGCCGCG TCGATTTGTG CGACCTTCCT TTGGTAACGA
851 TAGACGGCGA AACGGCGCGC GATTTGACG ACGCGGTGTT TGCCGAAAAA
901 GTCGGACGCA ATTACCGCCT GGTCTGGCG ATTGCGGATG TCAGCCATTA
951 TGTCGCCCCT GACGATGCGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
1001 GCGGTATTTT CCCGCGCCGT ATGATTCCGA TGCTGCCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCCGATGTC GAGCGTTTGT GTATGGTGTG
1101 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGTTCTATC
1151 CCGCCGTGAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTTGGAAA
1201 TGCTTTTcAG ACGGCATCGG GAATCCGCAC AAAGCCCAA TCGACACGCT
1251 TTACAAGCTG TTTAAATTTT TGCAGAAAAA ACGTCTGGCG CGCGGGCGG
1301 TGAGATTTGA AAGCGTCGAA ACCCAGATGA TTTTCGACGA CAACGGCAAA
1351 ATCGAAAAAA TTGTCCCCGT CGTCCGCAAC gatGCCACA AGCTGATTGA
1401 AGAATGTATG CTGGCGGCGA ATGTTTGCGC GCGGATTTT CTGTTGAAAA
1451 ACAAAACATAC GGCTTTGTTT CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1501 CTCGCCACCC TGCAGGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1551 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GAACAATTCA
1601 AAGGCAGGCC GGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAGCAGGCGG TTTACGAACC GCATTGCGAA GGGCATTTCT GTTTGGCTTA
1701 TGAAGCATAC GCCCACTTTA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1751 CCGTCCACCG TGCCATCAAA GCCGTATTGA ACCGGAAGAA CTACACGCCA
1801 AACAAAAGCT GGCAGGCTTT GGGCGTGCAT ACTTCGTTTT GCGAACGCCG
1851 TGCCGACGAT GCTGGCCGCG ATGTGGAAAA CTGGCTGAAA ACTTATTATA
1901 TGCCGCGATAA GGTCCGTGAA ATATTTGAAG GcaaaatCtc ccggggtgtg
1951 gcaaaTtttg gaATATTTGT CACTTTGGAC GATATccata tcgacggtct
2001 ggtacaTATC AGCGatttgg gcgaAGATTA TTTCaacttc cgccccgAAA
2051 TCATGGCAAT CGAAGGCGAA CGCAGCGGCA TCCGTTTCAA TATGGGGGAC
2101 AGGGTTGCCG TCCGGGTCGC GCGTGCCGAT TTGGATGATG GAAAAATCGA
2151 CTTTGTCTTA ATTGCCGAG AAAGCGGCAG GCGGCGGAAG GTCAAATTAT
2201 CGGCATCTGC CAAACCGGCA GGGGCGGCGG GGAAAGGGAA ATCGAAAACC
2251 ACCGCCGAGA AAAAAACAGC CCGATGCGGC AAAGTAAGGG GAAGGGCGT
2301 GCCTGCCGTT GCCGAATCGG GGAAAAAGGC AAAGAAACCG GTTCCGATTA
2351 AGGTCAAAAA ACGGAAAGGC AAATCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2980; ORF 988.ng>:

g988.pep

```

1  MNKNIKSLNL REKDPFLSRE KORYEHPLPS REWIIELLER KGVPSKIESL
51  ARELSITEDE YVFFERRLKA MARDGQVLIN RRGAVCAADK LDLVKCRVEA
101 HKDGFGFVAV LMPMDEGDFV LYERQMRGVM HGDTVTVRPA GMDRRGRREG
151 TFLDIVERAQ SKVVGFRFYM RGVAILPED KRLNQSIVLE PDGVARFKPE
201 SGQVIVGKIE VYPEQNRPAV AKIIEVLGDY ADSGMEIEIA VRKHHLPHRF
251 SEACAKSAKK IPDHVRKSDL KGRVDLCDLP LVTIDGETAR DFDDAVFAEK
301 VGRNYRLVVA IADVSHYVRP DDAIDADAQE RSTSVYFPRR MIPMLPENLS
351 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK
401 WLSDGIGNPH KAQIDTLYKL FKILQKKRLA RGAVEFESVE TQMI FDDNGK
451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LATLREQLGL LGLQLGGGDN PSPKDYAALA EQFKGRPDAE LLQVMMLRSM
551 QQAVYEPHCE GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNRKTYTP
601 NKSQALGVH TSFCERRADD AGRDVENWLK TYMRDKVGE IFEGKISRGV
651 ANGFIVTLD DIHIDGLVHI SDLGEDYFNF RPEIMAIEGE RSGIRFNMGD
701 RVAVRVARAD LDDGKIDFVL IAGESGRRRK VKLSASAKPA GAAGKGSKT
751 TAEKKTARCG KVRGRGVPVAV AESGKKAKKP VPIKVKKRKG KS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2981>:

```
m988.seq (partial)
1  ..ACAGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
51  CTATATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
101 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
151 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
201 GCCGGCAGTG GCAAAAATCA TCGAAGTTT GGGCGATTAT GCCGACAGCG
251 GCATGGAGAT TGA AATTGCC GTGCGCAAGC ATCATTTGCC GCACCAATTC
301 AGTGAAGCGT GTGCCAAGC TCGCAAAAAA ATTCCCGTCC ATGTACGCAA
351 AAGCGATTTG AAAGGCCGCG TCGATTTGCG CGACCTGCCT TTGGTAACGA
401 TAGACGGCGA AACGGCGCGC GATTTGACG ACGCGGTGTT TGCCGAAAAA
451 GTCGGACGCA ATTACCGTCT GGTGCGTGGC ATTGCGGATG TCAGCCATTA
501 TGTCCGCCCT GACGATGTGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
551 GCGTATATTT CCCGCGCCGT GTGATTCCGA TGCTGCCGGA AAACCTGTCT
601 AACGGCATTT GCTCGCTCAA TCCCGATGTC GAGCGTTTGT GTATGGTGTG
651 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTACC
701 CCGCCGTAAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTTGGAAA
751 TGGATTTTCAG ACGGCATCGA CCATCCGTAC AAAGCCCAAA TCGACACCCT
801 TTACAAACTC TTCAAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGCGCGG
851 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGATGA CAACGGCAAA
901 ATCGAAAAAA TCGTCCCGGT TGTCCGCAAC GATGCCCACA AGCTGATTGA
951 AGAATGTATG CTGGCGGCGA ATGTTTGCGC AGCGGATTTT CTGTTGAAAA
1001 ACAAGCATAC GGCTTTGTTC CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1051 CTCGCCACCC TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1101 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGTC GAACAATTCA
1151 AAGGCAGACC TGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1201 CAGCAGGCGG TTTACGAACC GCATTGCGAC GGACACTTTG GTCTTGCCTA
1251 CGAAGCATAC GCCCACTTCA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1301 CCGTACACCG CGCCATCAAA GCCGTGTTGA ATCAGCAAAC CTACACGCCA
1351 AAAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1401 TGCCGACGAC GCCAGCCGCG ACGTGAAAAA CTGGCTGAAA ACCTATTATA
1451 TGCGCGATAA GGTGCGCGAA GTATTGGAAG GTAAAAATCTC CGGCATGACC
1501 AGTTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
1551 GCATATCAGC GATTTGGGCG AAGACTATTT CAACTTCCGC CCCGAAATCA
1601 TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTTCAACAT GGGGGACAGG
1651 GTTGCCGTCC GGGTCGCCCC TGCCGATTTG GATGACGGAA AAATCGATTT
1701 TGTCCTGATT GCCGGGGGGA GCGGCAGGGG GCGGAAAGTT AAATCATCCG
1751 CGTCTGCCAA ACCGGCAGGG ACGGCGGGGA AAGGGAAGCC GAAAACCGCC
```

1400

1801 GCCGAGAAAA AAACAGCCCG AGGCGGCAAA GTAAGGGGAA GGGGCGCGTC
 1851 TGCCGCCGCA GAATCGAGGA AAAAGGCAAA GAAACCGGTT CCGATTAAGG
 1901 TAAAAAACC GAAAGGCAAA TCATAA

This corresponds to the amino acid sequence <SEQ ID 2982; ORF 988>:

m988.pep (partial)

1 ..TVLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSIVLE PDGVAREFKPE
 51 SGQVIVGEIE VYPEQNRPAV AKIEVLGDY ADSGMEIEIA VRKHHLPHQF
 101 SEACAKAAK IPVHVRKSDL KGRVDLRDLP LVTIDGETAR DFDDAVFAEK
 151 VGRNYRLVVA IADVSHYVRP DDVIDADAQE RSTSVYFPRR VIPMLPENLS
 201 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK
 251 WISDGIDHPY KAQIDTLYKL FKILQKKRFE RGAVEFESVE TQMIFDDNGK
 301 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
 351 LATLREQLGL LGLQLGGGDN PSPKDYAALV EQFKGRPDAE LLQVMMLRSM
 401 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQOQTYTP
 451 KKSQWALGVH TSFCERRADD ASRDVENWLK TYMRDKVGE VFEGKISGMT
 501 SFGIFVTLDG IHIDGLVHIS DLGEDYFNFR PEIMAIEGER SGIRFNMGDR
 551 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGKPKTA
 601 AEKKTARGGK VRGRGASAAA ESRKKAKKPV PIKVKKRKGK S*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m988/g988 94.2% identity in 642 aa overlap

m988.pep				10	20	30
				TVLDIVERAQSKVVGRFYMDRGVAILEPED		
g988						
	130	140	150	160	170	180
m988.pep	40	50	60	70	80	90
	KRLNQSIVLEPDGVAREFKPESGQVIVGEIEVYPEQNRPAVAKIEVLGDYADSGMEIEIA					
g988						
	190	200	210	220	230	240
m988.pep	100	110	120	130	140	150
	VRKHHLPHQFSEACAKAAKIPVHVRKSDLKGRVDLRDLPVLTIDGETARDFDDAVFAEK					
g988						
	250	260	270	280	290	300
m988.pep	160	170	180	190	200	210
	VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFPRRVIPLMLPENLSNGICSLNPDV					
g988						
	310	320	330	340	350	360
m988.pep	220	230	240	250	260	270
	ERLCMVCDMVVITYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGIDHPYKAQIDTLYKL					
g988						
	370	380	390	400	410	420
m988.pep	280	290	300	310	320	330
	FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
g988						
	430	440	450	460	470	480
m988.pep	340	350	360	370	380	390
	LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALVEQFKGRPDAE					
g988						
	LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALAEQFKGRPDAE					

1401

	490	500	510	520	530	540
m988.pep	400	410	420	430	440	450
	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYTP					
g988	: : : : :					
	550	560	570	580	590	600
m988.pep	460	470	480	490	500	509
	KKSQWQALGVHTSFCERRADDASRDVENWLKTYYMRDKVGEVFEGKIS-GMTSFGIFVTLD					
g988	: : : : : :					
	610	620	630	640	650	660
m988.pep	510	520	530	540	550	569
	GIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVL					
g988	: : : : :					
	670	680	690	700	710	720
m988.pep	570	580	590	600	610	629
	IAGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAAESRKKA					
g988	: : : : :					
	730	740	750	760	770	780
m988.pep	630	640				
	VPIKVKRRKGKXS					
g988	:					
	VPIKVKRRKGKXS					
	790					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2983>:

```

a988.seq
1  ATGAATAAAA ATATTAAATC TTAAATTTA CGGGA AAAAG ACCCGTTTTT
51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTGCCCAGT CGGGAATGGA
101 TAATCGAGCT GCTTGAACGT AAAGGCGTAC CATCCAAGAT TGAAGCTTTG
151 GTACGCGAAT TGTCGATTAA GGAAGAAGAG TACGAATTTT TCGAACGTCG
201 TCTGAAGGCG ATGGCGCGGG ACGGTCAGGT TTTAATCAAC CGTCGGGGCG
251 CGGTTTGCGC GCGGACAAA TTGGATTGG TCAATGCCG TGTCAGGCG
301 CACAAAGACC GCTTCGGTTT CGCCGTGCCG CTCACGCCCG CCAAAGACCG
351 TGATTTTGTC TTGTACGAAC GCCAGATGCG CGGCATTATG CACGGCGATA
401 TTGTCACTGT TCGTCCTGCC GGCATGGACG GTAGGGGCCG CCGCGAAGGG
451 ACGGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
501 CTANATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
601 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
651 GCCGGCAGTG GCAAAAATCA TCGAAGTTTT GGGCGATTAT GCCGACAGCG
701 GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTTGCC GCACCAATTC
751 AGTGAAGCGT GTGCCAAAGC CGCGAAAAAA ATCCCGACC ATGTACGCAA
801 AAGCGATTG AAAGGCCGCG TCGATTGCG CGACCTGCCT TTGGTAACGA
851 TAGACGGCGA AACGGCTCGA GATTTTGACG ATGCGGTGTT TGCCGAGAAA
901 ATCGGACGCA ATTACCGTCT GGTCGTGGCG ATTGCCGATG TCAGCCATTA
951 TGTCCGCCCC GATGACGCTA TCGACACGGA CGCTCAGGAA CGCAGACCA
1001 GTGTTTACTT CCCGCGCCG GTGATTCCA GTTTGCCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCTCATGTC GAGCGTTTGT GTGTGGTGTG
1101 CGATATGGTT ATCACTTACG CGGGCAATAT CAAAGAATAC CGCTTCTACC
1151 CCGCCGTGAT GCGCTCTCAT GCGCGCTGA CCTACAACCA AGTTTGGA
1201 TGGCTTTCAG GCGGCATCGA GCATCCGTTT AAAACCCAAA TCGACACGCT
1251 TTACAACTC TTCAAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGGGCGG
1301 TGGAGTTTGA CAGCATCGAA ACCCAAATGC TTTTCGACGA CAACGGTAAA
1351 ATTGAAAAAA TCGTCCCCGT TGTCCGCAAC GATGCCACA AGCTGATTGA
1401 AGAATGTATG TTGGCGGCAA ACGTTTGCGC AGCGGATTTT CTGTTGAAAA
1451 ACAAGCATAC CGCATTGTTC CGCAACCATT TGGGGCCAC GCCCGAAAAA
1501 CTCGCCGCT TGCGCGAGCA GTCGGTCTG TTGGGGCTT AACTTGGCGG
1551 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GGACAGTTCA

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1601 AAGGCAGGCC GGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAACAGGCGG TTTACGAACC GCATTGCGAC GGACACTTTG GTCTTGCCTA
1701 CGAAGCATAC GCCCACTTCA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1751 CCGTACACCG CGCCATCAAA GCCGTGTTGA ATCAGCAAAC CTACACGCCA
1801 AAAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1851 TGCCGACGAC GCCAGCCGCG ACGTGGAAAA CTGGCTGAAA ACCTATTATA
1901 TGCGCGATAA GGTCGGCGAA GTATTCGAAG GTAAAATCTC CGGCATGACC
1951 AGTTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
2001 GCATATCAGC GATTGGGCG AAGACTATTT CAACTTCCGC CCCGAAATCA
2051 TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTCAACAT GGGGGACAGG
2101 GTTGCCGTCC GGGTCGCCCG TGCCGATTG GATGACGGAA AAATCGATT
2151 TGTCTGATT GCCGGGGGGA GCGGCAGGGG GCGGAAAGTT AAATCATCCG
2201 CGTCTGCCAA ACCGGCAGGG ACGGCGGGGA AAGGGAAGCC GAAACCGCC
2251 GCCGAGAAAA AAACAGCCCG AGGCGGCAAA GTAAGGGGAA GGGGCGCGTC
2301 TGCCGCCGCA GAATCGAGGA AAAAGGCAAA GAAACCGGTT CCGATTAAGG
2351 TAAAAAACG GAAAGGCAAA TCATAA

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This corresponds to the amino acid sequence <SEQ ID 2984; ORF 988.a>:

a988.pep

```

1 MNKNIKSLNL REKDPFLSRE KORYEHPLPS REWIIELLER KGVPSKIEAL
51 VRELSIKEEE YEFFERRLKA MARDGQVLIN RRGAVCAADK LDLVKCRVKA
101 HKDRFGFAVP LTPAKDGFV LYERQMRGIM HGDIVTVRPA GMDGRGRREG
151 TVLDIVERAQ SKVVGRFXMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
201 SGQVIVGEIE VYPEQNRPAV AKIIEVLGDY ADSGMEIEIA VRKHHLPHQF
251 SEACAKAAKK IPDHVRKSDL KGRVDLRDLP LVTIDGETAR DFDDAVFAEK
301 IGRNYRLVVA IADVSHYVRP DDAIDTDAQE RSTSVYFPRR VIPMLPENLS
351 NGICSLNPHV ERLCVVCDMV ITYAGNIKEY RFYPAVMRSH ARLTYNQVWK
401 WLSGGIEHPF KTQIDTLYKL FKILQKKRFE RGAVEFDSIE TQMLFDDNGK
451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LAALREQLGL LGLQLGGGDN PSPKDYAALA GQFKGRPDAA LLQVMMLRSM
551 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQQTYP
601 KKSQQALGVH TSFCERRADD ASRDVENWLK TYMRDKVGE VFEGKISGMT
651 SFGIFVTLTG IHIDGLVHIS DLGEDYFNFR PEIMAIEGER SGIRFNMGDR
701 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGKPKTA
751 AEKKTARGGK VRGRGASAAA ESRKKAKKPV PIKVKKRKGK S*

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m988/a988 97.0% identity in 641 aa overlap

```

m988.pep                                10      20      30
                                TVLDIVERAQSKVVGRFYMDRGVAILEPED
a988                                LYERQMRGIMHGDIVTVRPAGMDGRGRREGTVLDIVERAQSKVVGRFXMDRGVAILEPED
                                130      140      150      160      170      180

m988.pep                                40      50      60      70      80      90
                                KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA
a988                                KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA
                                190      200      210      220      230      240

m988.pep                                100      110      120      130      140      150
                                VRKHHLPHQFSEACAKAAKKIPVHVRKSDLKGRVDLRDLPVLTIDGETARDFDDAVFAEK
a988                                VRKHHLPHQFSEACAKAAKKIPDHVRKSDLKGRVDLRDLPVLTIDGETARDFDDAVFAEK
                                250      260      270      280      290      300

m988.pep                                160      170      180      190      200      210
                                VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFPRRVIPMLPENLSNGICSLNPDV
a988                                IGRNYRLVVAIADVSHYVRPDDAIDTDAQERSTSVYFPRRVIPMLPENLSNGICSLNPHV
                                310      320      330      340      350      360

m988.pep                                220      230      240      250      260      270
                                ERLCMVCDMVITYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGIDHPYKAQIDTLYKL
a988                                ERLCVVCDMVITYAGNIKEYRFYPAVMRSHARLTYNQVWKWLSGGIEHPFKTQIDTLYKL

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1403

	370	380	390	400	410	420
m988.pep	280	290	300	310	320	330
	FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
a988	FKILQKKRFERGAVEFDSIETQMLFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
	430	440	450	460	470	480
m988.pep	340	350	360	370	380	390
	LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALVEQFKGRPDAE					
a988	LLKNKHTALFRNHLGPTPEKLAALREQLGLLGLQLGGGDNPSPKDYAALAGQFKGRPDAE					
	490	500	510	520	530	540
m988.pep	400	410	420	430	440	450
	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYTP					
a988	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYTP					
	550	560	570	580	590	600
m988.pep	460	470	480	490	500	510
	KKSQWQALGVHTSFCERRADDASRDVENWLKTYMRDKVGEVFEGKISGMTSFGIFVTLTG					
a988	KKSQWQALGVHTSFCERRADDASRDVENWLKTYMRDKVGEVFEGKISGMTSFGIFVTLTG					
	610	620	630	640	650	660
m988.pep	520	530	540	550	560	570
	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI					
a988	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI					
	670	680	690	700	710	720
m988.pep	580	590	600	610	620	630
	AGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAAESRKKAKKPV					
a988	AGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAAESRKKAKKPV					
	730	740	750	760	770	780
m988.pep	640					
	PIKVKKRKGKXS					
a988	PIKVKKRKGKXS					
	790					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2985>:

g989.seq

1	ATGACCCCTT	TCACACTGAA	AAAAACCGTC	CTGCTGCTCG	GCACTGCCTT
51	TGCCGCCGCA	TCTGTCCACG	CATCCGGCTA	CCACTTCGGC	ACACAGTCGG
101	TCAACGCGCA	AAGCACGGCA	AATGCCGCCG	ACGCGTCGAC	CATCTTCTAC
151	AATCCCGCCG	GCCTGACCAA	ACTCGACAGC	AGCCAGATT	CCGTCAACGC
201	CAACATCGTG	CTGCCCAGCA	TTCATTATGA	AGCAGATTCC	GCCACCGACT
251	TTACCGGGCT	TCCCGTCCAA	GGTTCTAAAA	ACGGCAAAAT	CACCAAAACC
301	ACGGTCGCAC	CCCACATTTA	CGGCGCATAC	AAAGTCAACG	ACAATCTGAC
351	CGTGGGCTTG	GGCGTGTACG	TCCCCTTCGG	CTCTGCCACC	GAATACGAAA
401	AAGATTCCGT	GTTGCGCCAC	AACATCAACA	AACTCGGTCT	GACCAGCATC
451	GCCGTCGAAC	CTGTGCGCCG	GTGGAAACTC	AACGAACGCC	ATTCTTTCGG
501	CGCAGGCATC	ATCGCCCCAAC	ATAATTCCGC	CGAACTGCGC	AAATATGCCG
551	ACTGAGGAAT	CCCCAAAAAA	GCGCAAATGC	TGCAAGCAAC	ACCTTCTAAT
601	CCTACTGCCG	CTGCTCAAAT	CAAGGCCGAC	GGACACGCCG	ATGTCAAAGG
651	CAGCGATTGG	GGCGTCGGCT	ACCAACTGGC	GTGGATGTGG	GACATCAACG
701	ACCGCGCGCG	CGTGGGCGTG	AACTACCGTT	CCAAAGTTTC	ACACACGCTC
751	AAAGGCGATG	CCGAATGGGC	GGCAGACGGC	GCGGCGGCGA	AACAACAGTG
801	GAATGACAAT	ATGCTCACAC	CGCTCGGTTA	CACGGCGAAT	GAAAAAGCCA
851	GTGTCAAAAT	CGTAACGCCT	GAGTCTTTGT	CCGTACACGG	CATGTACAAA

1404

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901 GTGTCCGACA AAGCCGACCT GTTCGGCGAC GTAAC TTGGA CGCGCCACAG
951 CCGCTTCAAT AAGGCGGAAC TGT TTTTGA AAAAGAAAAA AATATTGCTA
1001 ATGGCAAAAA ATCCGACCGC ACCACCATCA CCCC AACTG GCGCAACACC
1051 TACAAAGTCG GCTTGGGCGG TTCTTATCAA ATCAGCGAAC CGCTGCAACT
1101 GCGCGTCGGC ATCGCTTTTG ACAAACCGCC TGTCCGCAAC GCCGACTacC
1151 GCATGAACAG CCTGCCCGAC GGCAACCGCA TCTGGTTCTC CGCCGCGCATG
1201 AAATACCATA TCGCAAAAAA CCACGTCGTC GATGCCGCCT ACACCCACAT
1251 CCACATCAAC GACACCAGCT ACCGCACGGC GAAGGCAAGC GGCAACGATG
1301 TGGACAGCAA AGGTGCGTCT TGC GCACGTT TCAAAAACCA CGCCGACATC
1351 ATCGGCCTGC AATACACCTA CAAATTCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2986; ORF 989.ng>:

g989.pep

```

1 MTPFTLKKTV LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAADASTIFY
51 NPAGLTKLDS SQISVNANIV LPSIHYEADS ATDFTGLPVQ GSKNGKITKT
101 TVAPHIYGAY KVNDNLTVGL GYVVPFGSAT EYEKDSVLRH NINKLGLTSI
151 AVEPVAAWKL NERHSFGAGI IAQHNSAELR KYAD*GIPKK AQMLQATPSN
201 PTAAAIKAD GHADVKGS DW GVG YQLAWMW DINDRARGV NYRSKVSHTL
251 KGDAEWAADG AAAKQQWNDN MLTPLGYTAN EKASVKIVTP ESLSVHGM YK
301 VSDKADLF GD VTWTRHSR FN KAELFF EKEK NIANGKSDR TTITPNWRNT
351 YKVG LGGSYQ ISEPLQLRVG IAFDKPPVRN ADYRMNSLPD GNRIWF SAGM
401 KYHIGKNHVV DAA YTHIHIN DTSYRTAKAS GNDVDSKGAS CARFKNHADI
451 IGLQYTYKFK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2987>:

m989.seq

```

1 ATGACCCCTT CCGCACTGAA AAAAACCGTC CTGCTGCTCG GCACTGCCTT
51 TGCCGCCGCA TCCGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
101 TCAACGCGCA AAGCACGGCA AATGCCGCCG CCGCAGAAGC CGCCGACGCA
151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAAACTCG ACAGCAGCCA
201 GATTTCCGTC AACGCCAACA TCGTGCTGCC CAGCATTCAT TATGAGGCGG
251 ATTCCGCCAC CGACTTTACC GGGCTTCCCG TCCAAGGTTG GAAAAGCGGC
301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTGG GCTTGGGCGT GTACGTCCCC TTCGGCTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGA AACTCAACGA
501 CCGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAAC
551 TGCGCAAATA TGCCGACTGG GGGATTAAGA GTAAAGCAGA GATATTGACG
601 GCAAAACCGC CCAAACCTAA CGGTGTAGCC GAAGCTGCAA AAATT CAGGC
651 CGACGGACAC GCCGATGTCA AAGGCAGCGA TTGGGGCTTC GGCTACCAAC
701 TGGCGTGGAT GTGGGACATC AACGACCGTG CGCGCGTGGG CGTGA ACTAC
751 CGTTCCAAAG TCTCGCACAC GCTCAAAGGC GATGCCGAAT GGGCGGCAGA
801 CGCGCGGCG GCGAAAGCAA TGTGGAGTAC GATGCTTGCA GCAAACGGCT
851 ACACGGCGAA TGAAAAAGCC CGCGTTAAAA TCGTTACGCC TGAGTCTTTG
901 TCCGTACACG GTATGTACAA AGTGTCCGAT AAAGCCGACC TGTTCCGGCGA
951 CGTAACTTGG ACGCGCCACA GCCGCTTCGA TAAGGCGGAA CTGGTTTTTG
1001 AAAAAGAAAA AACCGTCGTC AAAGGCAAAT CCGACCGCAC CACCATCACC
1051 CCAA ACTGGC GCAACACCTA CAAAGTCGGC TTCGGCGGTT CTTATCAAAT
1101 CAGCGAACCG CTGCAACTGC GCGCCGGCAT CGCTTTTGAC AAATCGCCCG
1151 TCCGCAACGC CGACTACCGC ATGAACAGCC TACCCGACGG CAACCGCATC
1201 TGGTCTCCG CCGGTATGAA ATACCATATC GGTAAAAACC ACGTCGTCGA
1251 TGCCGCTAC ACCACATCC ACATCAACGA CACCAGTAC CGCAGCGGA
1301 AGGCAAGCGG CAACGATGTG GACAGCAAAG GCGCGTCTTC CGCAGTTTC
1351 AAAAACCACG CCGACATCAT CGGTCTGCAA TACACCTACA AATTCAAATA
1401 A

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This corresponds to the amino acid sequence <SEQ ID 2988; ORF 989>:

m989.pep

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1 MTPSALKKTV LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAAAAEADA
51 STIFYNPAGL TKLDSSQISV NANIVLPSIH YEAD SATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLND R HS FGAGIIAQHT SAELRKYADW GIKSKAEILT
201 AKPPKPNGVA EAAKIADGH ADVKGS DWGF GYQLAWMWDI NDRARVGVNY
251 RSKVSHTLKG DAEWAADGAA AKAMWSTMLA ANGYTANEKA RVKIVTPESL
301 SVHGM YKVSD KADLF GDVTW TRHSRFDKAE LVFEKEKTVV KGKSDRTTIT

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351 PNWRNTYKVG FGGSYQISEP LQLRAGIAFD KSPVRNADYR MNSLPDGNRI
401 WFSAGMKYHI GKNHVVDAA YTHIHINDTSY RTAKASGNDV DSKGASSARF
451 KNHADIIGLQ YTYKFK*

Homology with a predicted ORF from *N. gonorrhoeae*

		10	20	30	40	50
g989.pep	MT	PFTLKKT	VLL	LGTAFAA	ASVHASGYHFGTQSVNAQSTANAA-----	DASTIFYNPAGL
		:				
m989	MT	PSALKKT	VLL	LGTAFAA	ASVHASGYHFGTQSVNAQSTANAAAAEA	DASTIFYNPAGL
		10	20	30	40	50 60
		60	70	80	90	100 110
g989.pep	TK	L	DSSQ	ISV	NANIVLPSI	HYEADSATDFTGLPVQGS
m989	TK	L	DSSQ	ISV	NANIVLPSI	HYEADSATDFTGLPVQGS
		70	80	90	100	110 120
		120	130	140	150	160 170
g989.pep	LT	VGLGVY	VPFGS	ATEYEK	D	SVLRHNINKLGLT
m989	LT	VGLGVY	VPFGS	ATEYEK	D	SVLRHNINKLGLT
		130	140	150	160	170 180
		180	190	200	210	220 230
g989.pep	SA	E	L	RKYAD	XGIPKKAQ	MLQATPSNPTA---AAQIKADGHADV
m989	SA	E	L	RKYAD	WGIKSKAE	ILTA
		190	200	210	220	230 240
		240	250	260	270	280 290
g989.pep	N	D	R	A	R	V
m989	N	D	R	A	R	V
		250	260	270	280	290
		300	310	320	330	340 350
g989.pep	L	S	V	H	G	M
m989	L	S	V	H	G	M
	300	310	320	330	340	350
		360	370	380	390	400 410
g989.pep	V	G	L	G	G	S
m989	V	G	F	G	G	S
	360	370	380	390	400	410
		420	430	440	450	460
g989.pep	A	Y	T	H	I	H
m989	A	Y	T	H	I	H
	420	430	440	450	460	

a989.seq

1	ATGACCCCTT	CCGCACTGAA	AAAAACCGTC	CTACTGCTCG	GCACTGCCTT
51	TGCCGCGCA	TCCGCACAAG	CCTCCGGCTA	CCACTTCGGC	ACACAGTCGG
101	TCAACGCGCA	AAGCACGGCA	AATGCCGCCG	CCGCAGAAGC	CGCCGACGCA
151	TCGACCATCT	TCTACAACCC	TGCCGGCCTG	ACCAAACTCG	ACAGCAGCCA
201	GATTTTCGTC	AACGCCAACA	TCGTGCTGCC	CAGCATTTCAT	TATGAGGCGG
251	ATTCCGCCAC	CGACTTTACC	GGGCTTCCCG	TCCAAGGTTTC	GAAAAGCGGC

1406

```
301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTAG GCTTGGGCGT GTACGTCCCC TTCGGTCTGT
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGA AACTCAACGA
501 ACGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAGC
551 TCGGCAAATA TGCCGACTGG GGGATTATGG AAAAAGCGAA AGCACTAAAA
601 GAAACACCCC CCAATCCAAC TAAAGCCGCC CAAATCAAAG CCGACGGACA
651 CGCCGATGTC AAAGGCAGCG ATTGGGGCTT CGGCTACCAA CTGGCGTGGA
701 TGTGGGACAT CAACGACCGT GCGCGCGTGG GCGTGAAC TA CCGTTCCAAA
751 GTCTCACACA CGCTCAAAGG CGATGCCGAA TGGGCGGCAG ACGACGCAAT
801 GGCGAAACAG TTATGGGATG CAAACAAACT CGCACTGCTC GGCTACACGC
851 CAAGCGAAAA AGCCCGCGTT AAAATCGTTA CGCCCGAGTC TTTGTCCGTA
901 CACGGTATGT ACAAAGTGTC CGACAAAGCC GACCTGTTCG GCGACGTAAC
951 TTGGACGCGC CACAGCCGCT TCGATAAGGC GGAAGTGGTT TTTGAAAAAG
1001 AAAAAACCAT CGTCAACGGC AAATCCGACC GCACCACCAT CACCCCAAC
1051 TGGCGCAACA CCTACAAAGT CGGCTTCGGC GGTCTTATC AAATCAGCGA
1101 ACCGCTGCAA CTGCGCGCCG GCATCGCTTT TGACAAATCG CCCGTCCGCA
1151 ACGCCGACTA CCGCATGAAC AGCTGCCCCG ACGGCAACCG CATCTGGTTC
1201 TCCGCCGCGA TGAAATACCA TATCGGCAAA AACCACGTCG TCGATGCCGC
1251 CTACACCCAC ATCCACATCA ACGACACCAG CTACCGCACG GCGAAGGCAA
1301 GCGGCAACGA TGTGGACAGC AAAGGCGCGT CTTCCGCACG TTTCAAAAAC
1351 CACGCCGACA TCATCGGCCT GCAATACACC TACAAATTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2990; ORF 989.a>:

a989.pep

```
1 MTPSALKKTV LLLGTAFAAA SAQASGYHFG TQSVNAQSTA NAAAAEAADA
51 STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYK VNDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNERHS FGAGIIAQHT SAELRKYADW GIMEKAKALK
201 ETFPNPTKAA QIKADGHADV KGS DWGFGYQ LAWMWDINDR ARVGVNYRSK
251 VSHTLKGDAE WAADDAMAKQ LWDANKLALL GYTPSEKARV KIVTPESLSV
301 HGMVKVSDKA DLFGDVTWTR HSRFDKAE LV FEKEKTIVNG KSDRTTITPN
351 WRNTYKVGFG GSYQISEPLQ LRAGIAFDKS PVRNADYRMN SLPDGNRIWF
401 SAGMKYHIK NHVVDAAATH IHINDTSYRT AKASGNDVDS KGASSARFKN
451 HADIIGLQYT YKFK*
```

m989/a989 93.1% identity in 467 aa overlap

```
10 20 30 40 50 60
m989.pep MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a989 MTPSALKKTVLLLGTAFAAASQAQASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL
10 20 30 40 50 60

70 80 90 100 110 120
m989.pep TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYK VNDN
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a989 TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYK VNDN
70 80 90 100 110 120

130 140 150 160 170 180
m989.pep LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNDRHSFGAGIIAQHT
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a989 LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSFGAGIIAQHT
130 140 150 160 170 180

190 200 210 220 230 240
m989.pep SAELRKYADWGIKSKAEILTAKPPKPNGVAEAAKIQADGHADVKGSDWGFGYQLAWMWDI
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a989 SAELRKYADWGIMEKAKALKETFPNPNT---KAAQIKADGHADVKGSDWGFGYQLAWMWDI
190 200 210 220 230

250 260 270 280 290 299
m989.pep NDRARVGVNYRSKVSHTLKGDAEWAADGAAAKAMW-STMLAANGYTANEKARVKIVTPES
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a989 NDRARVGVNYRSKVSHTLKGDAEWAADDAMAKQLWDANKLALLGYTPSEKARVKIVTPES
```

1407

	240	250	260	270	280	290
m989.pep	300	310	320	330	340	350
	LSVHGMVKVSDKADLFQDVTWTRHSRFDKAELVFEKEKTVVKGKSDRTTITPNWRNTYKV					
a989	LSVHGMVKVSDKADLFQDVTWTRHSRFDKAELVFEKEKTIIVNGKSDRTTITPNWRNTYKV					
	300	310	320	330	340	350
m989.pep	360	370	380	390	400	410
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
a989	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
	360	370	380	390	400	410
m989.pep	420	430	440	450	460	
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					
a989	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					
	420	430	440	450	460	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2991>:

```

m990.seq
1  ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCCTACCA AAATCGGCGA
51  CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCAT
101 ATTTTTCAG CGGTAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAATTACAAT AGCGGCATCC TCGCGTCTGA
201 TAATATGCCC GTTGTCAAAA AATATATTAC AGAGAAGTAT GGGGCTGATT
251 TAAAGCAGGC GGTAAAAAGT CAATTACAGG ATTTATACAA AACAAGACCG
301 GAAGCTTGGG CAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGCACA
351 GTTTGGAACA AAATTTAGTA CGCTCAAACA GACGATGCCC GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCCAC GTCGCCGGAC AGGTGTTTGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TACGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCCTGAAC ACGAAAGATG AAAAAGTGAC
651 CGTCCATAAG GATTATGCGG GCGGCGCGGA TTTCTGTTC GGCTACGACG
701 TGCGGGAGTC GGACGAACCC GCCCTGACCT TTGAAGACAA AGTCAGCGGA
751 CAATCCGGCG TGGTTTTTGA ACGCCGGCCG GAAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CAAAACGGC GGATTCCGGT TCGTTTGGT
851 TTAAACAAAA TTACCGGCAG GGACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCCAAC AGGCTTATGC GGCAAATACT TTGTTGGGC
1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCCCT
1051 CAAAAATTGT GGCTGCGCTT CATCGGCGGC CGGTCCGATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GGTGGCGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GACTGGCAAT CCGCGTGATG
1201 GGCAGGAGG CCGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTGAT TTGTATGGTT ATGGCGGGGG TGTTTATGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCGG AACGCTACAA
1401 AACCAGAGGT TGGACGGCTT CTGTCGAAGG CGGCTACAAC GCGCTTGTGG
1451 CGGAAGGCAT TGTGCGAAAA GGCAATAATG TCGGTTTTTA CCTACAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GCGGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCGGCAGCGG TCAGTGGCAA AGCGCGCCG
1601 GCATTGCGGC AAAAACCCTT TTTGCTTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGCCG CTTTTAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCA CTCGAAGGGC
1751 GGTTCGGTAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TATGGCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAATG
1851 GCTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2992; ORF 990>:

m990.pep

```

1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGNKYN SGILAVDNMP VVKKYITEKY GADLKQAVKS QLQDLYKTRP
101 EAWAENKKRT EEAYIAQFGT KFSTLKQTMP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHTLE
201 TSDNARIRLN TKDEKLTVHK DYAGGADFLF GYDVRESDEP ALTFEDKVSQ
251 QSGVVLERRP ENLKTLDGRK LIAAKTADSG SFAFKQNYRQ GLYELLKQKC
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGWRKGVQ IGGEVFVRQN EGSRLAIGVM
401 GGRAGQHASV NGKGAAGSD LYGYGGGVYA AWHQLRDKQT GAYLDGWLQY
451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGIVGK GNNVRFYLPQ
501 QAQFTYLGVN GGFTDSEGT VLLGSGQWQ SRAGIRAKTR FALRNGVNLQ
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
601 YGKRTDGDKE AALSLKWL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2993>:

```

a990.seq
1 ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCGA
51 CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTTCAG CCGTAAAACC GATCAAAAT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAATAACAAT AGCGGCATAC TCGCCGTCGA
201 TAATATGCCC GTTGTTAAGA AATATATTAC AGATACTTAC GGGGATAATT
251 TAAAGGATGC GGTAAAGAG CAATTACAGG ATTTATACAA AACAAGACCC
301 GAAGCTTGGG AAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGAACA
351 GCTTGGACCA AAATTTAGTA TACTCAAACA GAAAAACCCG GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCGAC GTCGCCGGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TATGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCCTGAAC ACGAAAGATG AAAAAGTAC
651 CGTCCATAAA GCGTATCAGG GCGGTGCGGA TTTCTGTTC GGCTACGACG
701 TGCGGGAGTC GGACAAACCC GCCCTGACCT TTGAAGAAAA AGTCACGGGA
751 CAATCCGCGC TGGTTTTGGA ACGCCGGCCG GAAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CGGAAAAGGC AGACTCTAAT TCGTTTGCCT
851 TTAAACAAAA TTACCGGCAG GGACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCAAC AGGCTTATGC GGCAAATACT TTGTTCCGGC
1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCCGT
1051 CAAAATTGT GGCTGCGCTT CATCGGCGGC CGGTGCGATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GCGGCGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GGCTGGCAAT CCGCGTGATG
1201 GCGGCGAGGG CTGGCCAGCA CGCATCAGT AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTTAT TTGCATGTTT ATGGCGGGGG TGTATTATGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCGG AACGCTACAA
1401 AACCAGGCT TGGACGGCTT CTGTGCAAGG CCGCTACAAC GCGCTTGTGG
1451 CGGAAGGCGT TGTGCGAAAA GGCAATAATG TGCGGTTTTA CCTGCAACCG
1501 CAGGCGCAGT TTACTTACTT GGGCGTAAAC GCGGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCGGCAGCGG TCAGTGGCAA AGCCGCGCCG
1601 GCATTCCGGC AAAAACCCGT TTTGCTTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGCCG CTTTTAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCG CTCGAAGGGC
1751 GGTTCCGCAT TGAAGCCGGT TGGAAGGCC ATATGTCCGC ACGCATCGGA
1801 TACGGCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAAATG
1851 GCTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2994; ORF 990.a>:

```

a990.pep
1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGNKYN SGILAVDNMP VVKKYITDLY GDNLKDAVKK QLQDLYKTRP
101 EAWAENKKRT EEAYIEQLGP KFSILKQKNP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHMLE
201 TSDNARIRLN TKDEKLTVHK AYQGGADFLF GYDVRESDEP ALTFEELKVSQ
251 QSGVVLERRP ENLKTLDGRK LIAAEKADSN SFAFKQNYRQ GLYELLKQKC
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGRRKGVQ IGGEVFVRQN EGSRLAIGVM

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1409

401 GGRAGQHASV NGKGGGAAGSY LHGYGGGVYA AWHQLRDKQT GAYLDGWLQY
451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGVVGK GNNVRFYLQP
501 QAQFTYLGVN GGFTDSEGTA VGLLGSGQWQ SRAGIRAKTR FALRNGVNLQ
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
601 YGKRTDGDKE AALSLKWLF*

m990/a990 96.0% identity in 619 aa overlap

	10	20	30	40	50	60
m990.pep	MFRAQLGSNTRSTKIGDDADFSFSKPKPGTSHYFSSGKTDQNSSEYGYDEINIQGKNYN					
a990	MFRAQLGSNTRSTKIGDDADFSFSKPKPGTSHYFSSGKTDQNSSEYGYDEINIQGKNYN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m990.pep	SGILAVDNMPVVKYITEKYGADLKQAVKSQLODLYKTRPEAWAENKKRTEEAYIAQFGT					
a990	SGILAVDNMPVVKYITDITYGDNLDKDAVKKQLQDLYKTRPEAWAENKKRTEEAYIEQLGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m990.pep	KFSTLKQTMFDPDLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK					
a990	KFSILKQKNPDLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m990.pep	MTLKDSLWEPRRHSDIHTLETSDNARIRLNTKDEKLTVHKDYAGGADFLFGYDVRESDEP					
a990	MTLKDSLWEPRRHSDIHMLETSDNARIRLNTKDEKLTVHKAYQGGADFLFGYDVRESDEP					
	190	200	210	220	230	240
	250	260	270	280	290	300
m990.pep	ALTFEDKVSGQSGVVLERRPENLKTLDGRKLIAAKTADSGSFQKQNYRQGLYELLKQC					
a990	ALTFFEEKVSGQSGVVLERRPENLKTLDGRKLIAAEKADSNSFQKQNYRQGLYELLKQC					
	250	260	270	280	290	300
	310	320	330	340	350	360
m990.pep	EGGFCLGVQRLAIPAEAVLYAQQAANTLFLGLRAADRGDDVYAADPSRQKLWLRFIGG					
a990	EGGFCLGVQRLAIPAEAVLYAQQAANTLFLGLRAADRGDDVYAADPSRQKLWLRFIGG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m990.pep	RSHQNIRGGAAADGWRKGVQIGGEVFVRQNEGSRLAIGVMGGRAGQHASVNGKGGGAAGSD					
a990	RSHQNIRGGAAADGRRKGVQIGGEVFVRQNEGSRLAIGVMGGRAGQHASVNGKGGGAAGSY					
	370	380	390	400	410	420
	430	440	450	460	470	480
m990.pep	LYGYGGGVYAAWHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN					
a990	LHGYGGGVYAAWHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN					
	430	440	450	460	470	480
	490	500	510	520	530	540
m990.pep	ALVAEGIVGKGNNVRFYLQPAQFTYLGVNGGFTDSEGTA VGLLGSGQWQSRAGIRAKTR					
a990	ALVAEGVVGKGNNVRFYLQPAQFTYLGVNGGFTDSEGTA VGLLGSGQWQSRAGIRAKTR					
	490	500	510	520	530	540
	550	560	570	580	590	600
m990.pep	FALRNGVNLQPF AAFNVLHRSKSGVEMDGEKQTLAGRTALEGRFGIEAGWKGHMSARIG					
a990	FALRNGVNLQPF AAFNVLHRSKSGVEMDGEKQTLAGRTALEGRFGIEAGWKGHMSARIG					

1410

	550	560	570	580	590	600
	610	620				
m990.pep	YGKRTDGDKEAALSLKWLFX					
a990	YGKRTDGDKEAALSLKWLFX					
	610	620				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2995>:

```

g992.seq
1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCC  TGTCGCTTTT  GGGCGCGTTG  GGTATACGG
101 GATATGACAG  TGAGGCGGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GGCACGTGAG  GGGACGTGGG  TTTTCACGCG  CCCGTTCGCC  GACGGGCATC
201 GGCAGAAATCC  GGCCACAGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGATACCCCT  TCACGTCATC  GACGCGGACG  GCGCGAAACA  TAAAATTCGG
301 ATGGCGTATA  TCGACGCACC  GGAGATGAAA  CAGGCTTACG  GTACACGTTT
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAGGG  TAGGAAAGTC  AGTGTACGTG
401 TGTTTGAAAC  CGACCGCTAT  CAGCGCGAAG  TGGCGCAGGT  ATCCGCCGGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGGCGG  CGTGGCATTG
501 TAAAAGTTAT  GCTAAGAAGC  AGCAGGATAA  GCGGATTTT  GCCGACTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAAGCT
601 AAAAAATCCG  AAGCGCCGTG  GCGGTACCGC  CGGGCAGGCA  GGAGCGGCGG
651 GGGCAATAAG  GATTGGATGG  ATTCGTGGG  CGAATGGTTG  GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2996 ORF 992.ng>:

```

g992.pep
1  MFRRHRHLKN  MQIKKIMKWL  PVALSLLGAL  GYTGVDSEAV  RTAVAVLDVL
51  GTAGDVGFDA  PVRRRASAKS  GHSYTGTVSK  VYDGDTLHVI  DGDGAKHKIR
101 MAYIDAPEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFETDRY  QREVAQVSAG
151 KTDNLNMQVQ  DGAAWHYKSY  AKEQQDKADF  ADYADAQIQ  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGGGNK  DWMDSVGEWL  GIW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2997>:

```

m992.seq
1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCC  TGTCGCTTTT  GGGTGCCTTG  GGTATACGG
101 GGTACGGCAG  CGAGGCGGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GGCGCGGCAG  GGGACGCGGG  TTCCGACGCG  CCCGCCGCC  GCCGAGCATC
201 GGCAGAAATCC  GGCCACCGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGACACCCCT  TCACGTTATC  GACGCGGACG  GCGCGAAACA  CAAAATCCGG
301 ATGGCGTATA  TCGACGCGCC  GGAGATGAAA  CAGGCTTACG  GCACGCGTTC
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAAGG  CAGGAAAGTC  AGCGTGCAGG
401 TGTTTCGATC  CGACCGCTAC  CAGCGCGAAG  TGGCGCAGGT  TTCTGTCGGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGGCGG  CGTGGCATTG
501 TAAAAGTTAT  GCTAAGAAGC  AGCAGGATAA  GCGGATTTT  GCCGATTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAAGCT
601 AAAAAATCCG  AAGCGCCGTG  GCGGTACCGC  CGAGCAGGCA  GGAGCGGCGG
651 GGGCAATAAG  GATTGGATGG  ATGCCGTGGG  CGAATGGTTG  GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2998; ORF 992>:

```

m992.pep
1  MFRRHRHLKN  MQIKKIMKWL  PVALSLLGAL  GYTGYSSEAV  RTAVAVLDVL
51  GAAGDAGSDA  PARRRASAKS  GHRYTGTVSK  VYDGDTLHVI  DGDGAKHKIR
101 MAYIDAPEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFETDRY  QREVAQVSAG
151 KTDNLNMQVQ  DGAAWHYKSY  AKEQQDKADF  ADYADAQIQ  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGGGNK  DWMDAVGEWL  GIW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 992 shows 96.1% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. gonorrhoeae*

m992/g992 96.1% identity in 233 aa overlap

1411

	10	20	30	40	50	60
m992.pep	MFRRHRHLKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
g992	MFRRHRHLKNMQIKKIMKWL PVALSLLGALGYTGYDSEAVRTAVAVLDVLGTAGDVGFDA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m992.pep	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
g992	PVRRRASAKSGHSYTGTVSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m992.pep	LRAAAEGRKVSVRVFD TDRYQREVAQVSVGKTDLNLMQVQDGAAWHYKSYAKEQQDKADF					
g992	LRAAAEGRKVSVRVFETDRYQREVAQV SAGKTDLNLMQVQDGAAWHYKSYAKEQQDKADF					
	130	140	150	160	170	180
	190	200	210	220	230	
m992.pep	ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDAVGEWLGIWX					
g992	ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMSVGEWLGIWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2999>:

```
a992.seq
1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCT  TGTCGCTTTT  GGGTGCCTTG  GGTATACGG
101 GGTACGGCAG  CGAGGCGGTG  CGGACGCGCG  TTGCCGTACT  CGACGTACTC
151 GGCAGCGCAG  GGGACGCGGG  TTCGACGCG  CCCGCCCGCC  GCCGAGCATC
201 GGCAGAAATCC  GGCCACCGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGACACCTT  TCACGTTATC  GACGGCGACG  GCGCGAAACA  CAAAATCCGG
301 ATGGCGTATA  TCGACGCGCC  GGAGATGAAA  CAGGCTTACG  GCACGCGTTC
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAAGG  CAGGAAAGTC  AGCGTCCGCG
401 TGTTCGACAC  CGACCGCTAC  CAGCGCGAAG  TGGCGCAGGT  TTCTGTCGGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGGCGG  CGTGGCATTG
501 TAAAAGTTAT  GCTAAAGAAC  AGCAGGATAA  GGCGGATTTT  GCCGATTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAGACT
601 AAAAAATCCG  AAGCGCCGTG  GCGGTACCGC  CGGGCAGGCA  GGAGCGGCGG
651 GGGCAATAAG  GATTGGATGG  ATGCCGTGGG  CGAATGGTTG  GGCATTTGGT
701 AA
```

This corresponds to the amino acid sequence <SEQ ID 3000; ORF 992.a>:

```
a992.pep
1  MFRRHRHLKN  MQIKKIMKWL  PVALSLLGAL  GYTGYGSEAV  RTAVAVLDVL
51  GAAGDAGSDA  PARRRASAKS  GHRYTGTVSK  VYDGD TLHVI  DGDGAKHKIR
101 MAYIDAPEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFD TDRY  QREVAQVSVG
151 KTDNLMQVQ  DGAAWHYKSY  AKEQQDKADF  ADYADAQIQ  A  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGGGNK  DWMDAVGEWL  GIW*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 992 shows 100.0% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. meningitidis*

a992/m992 100.0% identity in 233 aa overlap

	10	20	30	40	50	60
a992.pep	MFRRHRHLKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
m992	MFRRHRHLKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a992.pep	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
m992	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
	70	80	90	100	110	120
	130	140	150	160	170	180

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```

a992.pep    LRAAAEGRKVSVRVFDTRDYQREVAQVSVGKTDNLNQVQDGAAWHYKSYAKEQQDKADF
            |||
m992        LRAAAEGRKVSVRVFDTRDYQREVAQVSVGKTDNLNQVQDGAAWHYKSYAKEQQDKADF
            130      140      150      160      170      180

            190      200      210      220      230
a992.pep    ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDDAVGEWLGIX
            |||
m992        ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDDAVGEWLGIX
            190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3001>:

```

g993.seq
1   CTGAAAGTCG TATTGGGCAG TTTTCAAGGC CCTTTGGATC TGCTGCTCTA
51  CCTTATCCGC AAGCAGAACA TCGATGTTCT CGATATTCCG ATGGTGGAAA
101 TTACCGGGCA GTATCTGCAC TATATTGCC AAATGGAAGC CTATCAGTTT
151 GATTTGGCGG CGGAATATCT TTTGATGGCG GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAGGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCTGCG TTGCCTACGA GCAATGAAA
301 CTGGCGGCGC AGGGTTTGA CCGCTGCCG CGTGGCGGAC GGGATTTGCG
351 GTGGGCTTAC CTGCCGCTGG AAATTGCAGC CGAGACGAAG CTGCCCGAGG
401 TTTACATCGC CGATTTGATG CAGGCATGGT TGGGCATTCT TTCTCGGGCA
451 AAACATACGC GCAGCCACGA AGTAATCCAA GAAACCCTTT CCGTGCAGCG
501 GCAAATGACG GCAATCCTGC GCCGTTTGAA CGAACACGGG ATATGCAGGT
551 TTCACGCCCT GTTCAATCCC GAACAGGGCG CGGCTTACGT GATCGTCAAC
601 TTCATCGCCC TGTTGGAGCT TGCCAAAGAA GGATTGGTCG GAATCGTACA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTTCGGC ACACGGGGCG GCGCGCATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3002 ORF 993.ng>:

```

g993.pep
1   LKVLGSGFQG PLDLLLYLIR KQIDVLDIP MVEITGOYLH YIAQMEAYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTAEVD EADPRAELV RRLAYEQMK
101 LAAQGLDALP RGRDFAWAY LPLEIAAETK LPEVYIADLM QAWLGILSRA
151 KHTRSHEVIQ ETLSVRAQMT AILRRLNEHG ICRFHALFNP EQGAAYVIVN
201 FIALLELAKE GLVGIVQEDG FGEIRISLNH EGAHSDGIFG TRGGRDVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3003>:

```

m993.seq
1   TTGAAAGTCG TATTGGGCAG CTTCCAAGGC CCTTTGGATC TACTGCTGTA
51  TCTGATCCGC AAACAGAATA TCGACGTA CTGATATTCCG ATGGTGAAGA
101 TTACCGAGCA GTATCTGCAC TACATCGCCC AAATAGAAAC CTATCAGTTT
151 GATTTGGCGG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAAC CGTCGAAGAC GAAGAAGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCTGCG TGGCTTACGA ACAGATGAAG
301 CTGGCGGCGC AGGGTTTGA CCGCTGCCG CGAGCGGAC GGGATTTGCG
351 GTGGGCTTAC CTGCCGCTGG AAATTGCCGT CGAAGCCAAG CTGCCCGAAG
401 TCTATATTAC CGACTTGACG CAAGCGTGGC TGGGTATTTT GTCTCGGGCA
451 AAACACACGC GCAGCCACGA AGTAATCAA GAAACCATCT CCGTGCAGCG
501 GCAAATGACG GCAATCCTGC GCCGTTTGAA CGGACACGGA ATATGCAGGT
551 TTCACGACCT GTTCAATCCC AAACAGGGCG CGGCTTACGT GGTCTGCAAC
601 TTCATCGCAC TGTTGGAGCT TGCCAAAGAA GGATTGGTCA GAATCGTGCA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTCCGGC ACACGAGGCG GCGCGCATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3004; ORF 993>:

```

m993.pep
1   LKVLGSGFQG PLDLLLYLIR KQIDVLDIP MVKITEQYLH YIAQIETYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTETVED EADPRAELV RRLAYEQMK
101 LAAQGLDALP RGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLGILSRA
151 KHTRSHEVIK ETISVRAQMT AILRRLNGHG ICRFHDLFNP KQGAAYVVVN
201 FIALLELAKE GLVRIVQEDG FGEIRISLNH EGAHSDGISG TRGGRDVF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 993 shows 93.1% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. gonorrhoeae*

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m993/g993 93.1% identity in 248 aa overlap

m993.pep	10	20	30	40	50	60
	LKVVLSFGQPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQ	IETYQFDLAAEYLLMA			
g993	10	20	30	40	50	60
	LKVVLSFGQPLDLLLYLIRKQ	NIDVLDIPMVEITGQYLHYIAQ	MEAYQFDLAAEYLLMA			
m993.pep	70	80	90	100	110	120
	AMLIEIKSRLLLPR	TETVEDEEADPRAELVR	RLAYEQMKLAAQGLDAL	PRAGRDFAWAY		
g993	70	80	90	100	110	120
	AMLIEIKSRLLLPR	TEAVEDEEADPRAELVR	RLAYEQMKLAAQGLDAL	PRAGRDFAWAY		
m993.pep	130	140	150	160	170	180
	LPLEIAVEAKLPEVYITDLTQ	AWLGILSR	AKHTRSHEVIKETISVRAQMTAILRRLN	GHG		
g993	130	140	150	160	170	180
	LPLEIAAETKLPEVYIADLMQ	AWLGILSR	AKHTRSHEVIQETLSVRAQMTAILRRLN	EHG		
m993.pep	190	200	210	220	230	240
	ICRFHDLFNP	KQGAAYVVVNFIALLELAKEGLVR	IVQEDGFGEIRISLNHEGAHSDG	ISG		
g993	190	200	210	220	230	240
	ICRFHALFNP	EQGAAYVIVNFIALLELAKEGLVG	IVQEDGFGEIRISLNHEGAHSDG	IFG		
m993.pep	249					
	TRGGRDVFX					
g993	249					
	TRGGRDVFX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3005>:

a993.seq

1	CTGAAAGTCG	TATTGAGCAG	TTTCAAGGC	CCTTTGGATC	TGCTGCTCTA
51	CCTTATCCGC	AAGCAGAACA	TCGATGTTCT	CGATATTCCG	ATGGTGAAGA
101	TTACCGAACA	GTATCTGCAC	TACATCGCCC	AAATAGAAAC	CTATCAGTTT
151	GATTTGCGCG	CGGAATATCT	TTTGATGGCA	GCAATGCTGA	TTGAAATCAA
201	ATCGCGCCTG	CTGCTGCCGC	GTACCGAAAC	CGTCGAAGAC	GAAGAAGCCG
251	ACCCGCGTGC	CGAGTTGGTG	CGCCGCCTGC	TGGCTTACGA	GCAGATGAAG
301	CTGGCGGCAC	AAGGGTTGGA	TGCGCTTCCT	CGTGCGGGCC	GGGATTTCGC
351	ATGGGCATAC	CTGCCACTGG	AAATTGCCGT	CGAAGCCAAG	CTGCCCGAAG
401	TCTATATTAC	CGACTTGACG	CAGGCGTGGC	TGAGTATTTT	GTCTCGGGCA
451	AAACATACGC	GCAGCCACGA	AGTTATCAAA	GAAACCATCT	CCGTGCGCGC
501	GCAAATGACG	GCAATCCTGC	GCCGTTTGAA	CAAACACGGG	ATATGCAGGT
551	TTACCGACCT	GTTCAATCCC	GAACAGGGCG	CGGCTTACGT	GGTCGTCAAC
601	TTATCGCAC	TGTTGGAGCT	TGCCAAAGAA	GGTTTGGTCG	GAATCGTACA
651	GGAAAGTCGT	TTCGAGAGAA	TCCGAATCAG	CCTCAATCAT	GAGGGGGCGC
701	ATTACAGACG	CATTTCGGC	ACACGGGGCG	GGCGCGATGT	GTTCTAA

This corresponds to the amino acid sequence <SEQ ID 3006; ORF 993.a>:

a993.pep

1	LKVVLSFGQ	PLDLLLYLIR	KONIDVLDIP	MVKITEQYLH	YIAQIETYQF
51	DLAAEYLLMA	AMLIEIKSRL	LLPRTETVED	EEADPRAELV	RRLAYEQMK
101	LAAQGLDALP	RAGRDFAWAY	LPLEIAVEAK	LPEVYITDLT	QAWLSILSRA
151	KHTRSHEVIK	ETISVRAQMT	AILRRLNKHG	ICRFHDLFNP	EQGAAYVVVN
201	FIALLELAKE	GLVGIVQEVG	FGEIRISLNH	EGAHS	SDGISG TRGGRDVF*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 993 shows 97.6% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. meningitidis*

a993/m993 97.6% identity in 248 aa overlap

a993.pep	10	20	30	40	50	60
	LKVVLSFGQPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQ	IETYQFDLAAEYLLMA			
m993	10	20	30	40	50	60
	LKVVLSFGQPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQ	IETYQFDLAAEYLLMA			

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	10	20	30	40	50	60
a993.pep	70	80	90	100	110	120
m993	70	80	90	100	110	120
a993.pep	130	140	150	160	170	180
m993	130	140	150	160	170	180
a993.pep	190	200	210	220	230	240
m993	190	200	210	220	230	240
a993.pep	249					
m993	249					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3007>:

g996.seq

```

1  ATGAACAGAA  GAACCTTCCT  CCTCGGCGCA  GCGCGTTGCG  TTCTTACCGC
51  CTGCGGCAGA  AAATCCGCCC  GAACCCACGC  CAAAATTCCC  GAAGGAAGCA
101 CCGTGCTTGC  CTTGGGCGAT  TCGCTCACCT  TCGGCTACGG  AGCAAACCCC
151 GCGGAATCCT  ACCCGCGCGA  ACTGCAAAAA  CTGACGGGTT  GGAATATTGT
201 CAACGGCGGC  GTATCGGGCG  ATACGTCCGC  GCAAGCCCTA  TCGCGCCTGC
251 CCGCGCTGTT  GGCACGCAAA  CCCAAGCTTG  TGATTGTCGG  CATAGGCGGC
301 AACGACTTTC  TCGCGCAAAGT  TCCCGAGGAG  CAGACCCGCG  CCAATATCGC
351 GAAAATCATC  GAAACCGTGC  AAAAGGAAAA  CATTCCTGCC  GTCTTCGTCG
401 GCGTGCCGCA  CATCACACTG  GCGCGTTTGT  TCGGGCATT  GAGCGACCAT
451 CCGCTGTATG  AGGATTTGTC  CGAGGAATAC  GGCATTCCGT  TGTTCGGCGG
501 CCGTGCGGCG  GAAATTTTGG  GCAATAATAA  TCTGAAATCC  GACCAAATCC
551 ACGCCAACGG  CAAAGGCTAT  CGGAAATTCG  CCGAAAATTT  GAATCAATTT
601 TTGAGAAAAC  ATGGGTTTAG  ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3008 ORF 996.ng>:

g996.pep

```

1  MNRRTFLLGA  GALLLTACGR  KSARTHAKIP  EGSTVLALGD  SLTFGYGANP
51  GESYPAQLQK  LTGWNIVNGG  VSGDTSQAAL  SRLPALLARK  PKLVIVGIGG
101 NDFLRKVPPE  QTRANIAKII  ETQKENIPA  VLVGVPHITL  GALEGHLSDH
151 PLYEDLSEYY  GIPLFGGAWA  EILGNNNLKS  DQIHANGKGY  RKFAENLNQF
201 LRKHGFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3009>:

m996.seq

```

1  ATGAACAGAA  GAACCTTCCT  CCTCGGCGCA  GCGCGTTGCG  TGCTTACCGC
51  CTGCGGCAGA  AAATCCGCCC  GAACCCACGC  CAAAATTCCC  GAAGGAAGCA
101 CCGTACTTGC  CTTGGGCGAT  TCGCTTACCT  TCGGCTACGG  CGCAAACCTT
151 GCGGAATCCT  ACCCGCGCGA  ACTGCAAAAA  CTGACGGGTT  GGAATATTGT
201 CAACGGCGGC  GTATCGGGCG  ATACATCTGC  CCAAGCCCTG  TCGCGCCTGC
251 CCGCGCTGTT  GGCACGCAAA  CCCAAGCTTG  TGATTGTCGG  CATAGGCGGC
301 AACGACTTTC  TCGCGCAAAGT  TCCCAAGGAG  CAGACCCGCG  CCAATATCGC
351 GAAAATCATC  GAAACCGTGC  AGAAGGAAAA  CATCCCGGCC  GTCTTCGTCG
401 GCGTGCCGCA  CATCACACTG  GGTGCGTTGT  TCGGGCATT  GAGCGATCAT
451 CCGCTGTATG  AGGATTTGTC  CGAGGAATAC  GGCATTCCGC  TGTTCGGCGG
501 CCGTGCGGCG  GAAATTTTGG  GCGATAATAA  TCTGAAATCC  GACCAAATCC
551 ACGCCAACGG  CAAAGGCTAT  CGGAAATTCG  CCGAAGATT  GAATCAATTT
601 TTGAGAAAAC  AGGGGTTTAG  ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3010; ORF 996>:

m996.pep

```

1  MNRRTFLLGA  GALLLTACGR  KSARTHAKIP  EGSTVLALGD  SLTFGYGANP
51  GESYPAQLQK  LTGWNIVNGG  VSGDTSQAAL  SRLPALLARK  PKLVIVGIGG

```

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101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSDH
 151 PLYEDLSEY GIPFGGAWA EILGDNLNKS DQIHANGKGY RKFAEDLNQF
 201 LRKQGFR

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 996 shows 98.1% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. gonorrhoeae*

m996/g996 98.1% identity in 207 aa overlap

m996.pep	10	20	30	40	50	60
	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQK					
g996						
	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQK					
	10	20	30	40	50	60
m996.pep	70	80	90	100	110	120
	LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII					
g996						
	LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII					
	70	80	90	100	110	120
m996.pep	130	140	150	160	170	180
	ETVQKENIPAVLVGVPHITLALFGHLSHDHPLYEDLSEYGIPLFGGAWAEILGDNLNKS					
g996						
	ETVQKENIPAVLVGVPHITLALFGHLSHDHPLYEDLSEYGIPLFGGAWAEILGNNLNKS					
	130	140	150	160	170	180
m996.pep	190	200				
	DQIHANGKGYRKFAEDLNQFLRKQGFR					
g996						
	DQIHANGKGYRKFAENLNQFLRKHGFRX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3011>:

a996.seq

1	ATGAACAGAA	GAACCTTCCT	CCTCGGCGCA	GGCGCGTTGC	TCCTTACCGC
51	CTGCGGCAGA	AAATCCGCCC	GAACCCACGC	CAAAATTCCC	GAAGGAAGCA
101	CCGTACTTGC	CTTGGGCGAT	TCGCTTACCT	TCGGCTACGG	CGCAAACCCC
151	GGCGAATCCT	ACCCCGCGCA	ACTGCAAAAA	CTGACGGGTT	GGAATATTGT
201	CAACGGCGGC	GTATCGGGCG	ATACATCCGC	CCAAGCCCTG	TCGCGCCTGC
251	CCGCGCTGTT	GGCACGCAAA	CCCAAGCTTG	TGATTGTCGG	CATAGGCGGC
301	AACGACTTTC	TGCGCAAAGT	TCCCAAGGAG	CAGACCCGCG	CCAATATCGC
351	GAAATCATC	GAAACCGTGC	AGAAGGAAAA	CATCCCCGCC	GTCTCGTTCG
401	GCGTGCCGCA	CATTACCTTG	GGCGCGTTGT	TCGGGCATT	GAGCGATCAT
451	CCGCTGTATG	AGGATTGTGC	CGAGGAATAC	GGCATTCCGC	TGTTCCGCGG
501	CGCGTGGGCG	GAAATTTTGG	GCGATAATAA	TCTGAAATCC	GACCAAATCC
551	ACGCCAACGG	CAAAGCTAT	CGGAAATTG	CCGAAGATT	GAATCAATTT
601	TTGAGAAAAC	AGGGTTTAG	ATAA		

This corresponds to the amino acid sequence <SEQ ID 3012; ORF 996.a>:

a996.pep

1	MNRRTFLLGA	GALLLTACGR	KSARTHAKIP	EGSTVLALGD	SLTFGYGANP
51	GESYPAQLQK	LTGWNIVNGG	VSGDTSQAAL	SRLPALLARK	PKLVIVGIGG
101	NDFLRKVPKE	QTRANIAKII	ETVQKENIPA	VLVGVPHITL	GALFGHLSDH
151	PLYEDLSEY	GIPFGGAWA	EILGDNLNKS	DQIHANGKGY	RKFAEDLNQF
201	LRKQGFR*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 996 shows 100.0% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. meningitidis*

a996/m996 100.0% identity in 207 aa overlap

a996.pep	10	20	30	40	50	60
	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQK					

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```

|||||
m996      MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQLOK
              10      20      30      40      50      60

              70      80      90      100     110     120
a996.pep   LTGWNIVNGGVSGD TSAQALSRLPALLARKPKLVIVIGGNDFLRKVPKEQTRANIAKII
|||||
m996      LTGWNIVNGGVSGD TSAQALSRLPALLARKPKLVIVIGGNDFLRKVPKEQTRANIAKII
              70      80      90      100     110     120

              130     140     150     160     170     180
a996.pep   ETVQKENIPAVLVGVPHITLGFHLSHDHPLYEDLSEEGYIPLFGGAWAEILGDNNLKS
|||||
m996      ETVQKENIPAVLVGVPHITLGFHLSHDHPLYEDLSEEGYIPLFGGAWAEILGDNNLKS
              130     140     150     160     170     180

              190     200
a996.pep   DQIHANGKGYRKFAEDLNQFLRKQGFRR
|||||
m996      DQIHANGKGYRKFAEDLNQFLRKQGFRR
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3013>:

```

g997.seq (partial)
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51  CTGGGCGCGC TTGTCCGCCG CCGTCACCTT GCGCGCGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GAAGGCGCGC CACACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGGCGTGT TGCGCCTGAT GAAAACCATC GGTTCGAGAC
251 CCCGTGCCGC CTTTGTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCCCGCG CCGCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AAACGTGCTTG
401 CCGATATGTC CGATTGTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTTGCAC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCAGTTTGGT CAGCCCTTGG TCTGGGGCGC GCTCAACACG CCTTTGGAAA
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GACGCGACTA TCTCCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCCGCTTGG CCGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAGC GCGCGTATGC CGTCTGAACA CCCTCCCGGA CGGAAAAGTC
751 TCGCTCAACG CGGAAGCCTT CGATGCCGCC ATACTTGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 CCGCAACCCG TCCGcCTGcC CGCCCGCTG ACcGGCATgC CCGAcggcAC
951 ggcCaatgG CTGCTTTgcc cgGGCAGGC tccggactgc CcccaaAacg
1001 aagTCTCCGC cGTCAtagc GTTCCGAcc GCGtcggcgC Gtttgcaaac
1051 cga...

```

This corresponds to the amino acid sequence <SEQ ID 3014 ORF 997.ng>:

```

g997.pep (partial)
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51  GNTDGFGLD NGQHILLGAY RGVRLRMKTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPSAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKORN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSDGVL
201 KKSQSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA ILATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGIADGTAQW LLCPGQAPDC PQNEVSAVIS VSDRVGAFAN
351 R....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3015>:

```

m997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51  CTGGGCGAGG CTGTCCGCCG CCGTCACCTT GCGCGCGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GCAGGCGCGC CACACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGGCGTGT TGCGCCTGAT GAAAACCATC GGTTCGGATC
251 CCCGTGCCGC CTTTGTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCCCGCG CCGCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGTG CACCGACTGC ATTCAAAGCC AAACGTGCTTG
401 CCGATATGTC CGATTGTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTGAT
501 GCAGTTTGGT CAGCCCTTGG TTTGGGGCGC GCTCAACACG CCTTTGGAAA

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1417

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551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAGCAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCCGCCCTGG CGGATCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCCTCCCGGA CGGGAAAGTG
751 CTCGTCAACG GCGAAGCTTT CGATGCCGCC GTCCCGGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAC CAGCCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGCCGTGC CGCCCCGCTG ACCGGCCTTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGGCAGGCT CGGACTGCCT GAAAACGAAG
1001 TGTCCGCCGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCGTGGGCGG ACAAAGCCCA CGCCGACCTC AAACGCATCC TTCCGCATTT
1101 GGGCGAACCC GAAGCCGTGC GCGTCATCAC CGAAAAACGC GCCACAACCG
1151 CAGCCGATGC CCCGCCGCG GACTTGTCT GGTTCACCG GCACCGCATC
1201 TTCCCCGCGG GCGACTACCT CCACCCGGAC TACCCGCCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 3016; ORF 997>:

m997.pep

```

1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51  GNTDGFGLD NGQHILLAGY RGVRLRMKTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRAPTAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSDGVL
201 KKS GSDYLLP KQDLGAIVAE PALADLQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGLADGTQVW LLCRGLGLP ENEVSAVISV SDRVGAFAFNR
351 AWADKAHADL KRILPHLGEP EAVRVITEKR ATTAADAPPP DLSWLHRHRI
401 FPAGDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 997 shows 96.0% identity over a 351 aa overlap with a predicted ORF (ORF 997) from *N. gonorrhoeae*

g997/m997 96.0% identity in 351 aa overlap

g997.pep	10	20	30	40	50	60
m997	10	20	30	40	50	60
g997.pep	70	80	90	100	110	120
m997	70	80	90	100	110	120
g997.pep	130	140	150	160	170	180
m997	130	140	150	160	170	180
g997.pep	190	200	210	220	230	240
m997	190	200	210	220	230	240
g997.pep	250	260	270	280	290	300
m997	250	260	270	280	290	300
g997.pep	310	320	330	340	350	
m997	310	320	330	340	350	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3017>:

```
a997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51  CTGGGCGGCG TTGTCCGCCG CCGTTACCTT GGCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCCCG CAGGCGGGCG GCAGGGCGCG CGCACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ATATTTTACT
201 CGGCGCATAC CGGGGCGTGT TCGCCTGAT GAAAACCATC GGTTCAGACC
251 CCCATGCCGC CTTTTTGC GC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCCCGCG CCCCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AACTGCTTG
401 CCGATATGTC CGATTTGCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCGC AATGGGTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCAGTTTTGG CAGCCCTTGG TTTGGGCGCG GCTCAACACG CCTTTGGAAA
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCCGCCCTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCATATGC CGTCTGAACA CCTCCCGGA CGGAAAGTG
751 CTCGTCAACG GCGAACCTTT CGATGCCGCC GTCCCGGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CTTTCGCTAT CACGCCATCA CCACCGTCTA TCTGCGCTAT
901 GCCGAACCCG TCCGCTTGCC TGCCCCGCTG ACCGGACTTG CCGACGGCAC
951 GGTGCAATGG CTGCTTGCC GGGGCAAGGCT CGGACTGCCT GAAAACGAAG
1001 TGTCCGCCGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCGTGGGCGG ACAAAGTTCA CGCCGACCTC AAACGCATCC TTCCGCATTT
1101 GGGCGAACCC GAAGCCGTGC GCGTCATCAC CGAAAAACGC GCCACAACCG
1151 CAGCCGATGC CCCGCCCGCG GATTGTGCTG GGTTCACCG GCACCGCATC
1201 TTCCCCGCGG GCGACTACCT CCACCCAGAC TACCCCGCCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA
```

This corresponds to the amino acid sequence <SEQ ID 3018; ORF 997.a>:

```
a997.pep
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARALA
51  GNTDGFGLD NGQHILLGAY RGVRLRMKTI GSDPHAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPFAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSDGVL
201 KKSQSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRIC RLNTLPDGKV
251 LVNGEPFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGLADGTQVQW LLCRGRLGLP ENEVSAVISV SDRVGAFANR
351 AWADKVHADL KRILPHLGEP EAVRVITEKR ATTAADAPPP DLSWLHRHRI
401 FPGADYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 997 shows 98.2% identity over a 437 aa overlap with a predicted ORF (ORF 997) from *N. meningitidis*

a997/m997 98.2% identity in 437 aa overlap

	10	20	30	40	50	60
a997.pep	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARALAGNTDGFGLD					
m997	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD					
	10	20	30	40	50	60
a997.pep	NGQHILLGAYRGVRLRMKTIGSDPHAAFLRVPLHWHMHGGGLQFRALPLPAPLHILGGVLL					
m997	NGQHILLGAYRGVRLRMKTIGSDPRAAFLRVPLHWHMHGGGLQFRALPLPAPLHILGGVLL					
	70	80	90	100	110	120
a997.pep	ARRVPSAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
m997	ARRAPTAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
	130	140	150	160	170	180
a997.pep	PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALELQRLGADIRLETRIC					
m997	PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALELQRLGADIRLETRIC					
	190	200	210	220	230	240
a997.pep	PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALELQRLGADIRLETRIC					
m997	PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALELQRLGADIRLETRIC					

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m997      PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPALADLQRLGADIRLETRVC
           190      200      210      220      230      240

           250      260      270      280      290      300
a997.pep  RLNTLPDGKVLVNGEPFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY
           |||||
m997      RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY
           250      260      270      280      290      300

           310      320      330      340      350      360
a997.pep  AEPVRLPAPLTGLADGTVQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKVHADL
           |||||
m997      AEPVRLPAPLTGLADGTVQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKAHADL
           310      320      330      340      350      360

           370      380      390      400      410      420
a997.pep  KRILPHLGEPEAVRVITEKRATTAADAPPPDLSWLHRHRIFFAGDYLHPDYPATLEAAVQ
           |||||
m997      KRILPHLGEPEAVRVITEKRATTAADAPPPDLSWLHRHRIFFAGDYLHPDYPATLEAAVQ
           370      380      390      400      410      420

           430
a997.pep  SGFASAEACLQSLSDAVX
           |||||
m997      SGFASAEACLQSLSDAVX
           430

```

g999.seq Not found yet

g999.pep Not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3019>:

```

m999.seq
1  ATGAATATGA AAAAATTGAT TTCCGCAATT TGTGTTTCAA TTGTTTTATC
51  AGCCTGCAAC CAACAATCAA AAACGGCACA AGCCGAAGAA CCTGTCCAAA
101 GTATCCAGGC TGCTGATTGT ACCGCCCCAA TGGACATCAC AGTTGAACAA
151 TATCTCATCA ATTTGGAGCA AGCATTTAAA ACTCAGAACG TCTCAACAAA
201 AATCCATAAT AAAAATATTG TCAAGACCGA TTGTGGTTAT GACCTTACTT
251 TGGTAATGGA TTTTGGGGCG ATTGCGCTCA AACTGGACGA GCAGCAAAAA
301 ATTAGAGCTA TCTCAGTAGG CTACATTTTA AAAACCGACG GAGAGAAAGG
351 ACAAAATCTA GTCAATAATG CCATAAATGG ATTACACAGT ATTCAGGCAG
401 TTCTGTCTTT AACTACCACA GACAAATTGG GCGAATCGGA AGCAGGAAAA
451 CAACTTTTTC CAGCTTTAAC CGAAGTCGTC AAAGAATCCA ATCAGACAGG
501 AGCAACAGCG CAAAAGACG TTCCGGCAGA TGGTATTTTA TATAGCGTTG
551 TTTTGA AAAA AGAAACAAAC ACCATTGCAA TAATCGGCAG AAAACAACCC
601 TAA

```

This corresponds to the amino acid sequence <SEQ ID 3020; ORF 999>:

```

m999.pep
1  MNMKKLISAI CVSIVLSACN QOSKTAQAE PVQSIQAADC TAPMDITVEQ
51  YLINLEQAFK TQNVSTKIHN KNIVKTDGKY DLTLMDFGA IALKLDEQOK
101 IRAISVGYIL KTDGEKGQNL VNNAINGLHS IQAVLSLTIT DKLGSEAGK
151 QLFTALTEVV KESNQTGATA QKDVPADGIL YSVVFEKETN TIAIIGRKQP
*

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a999.seq Not found yet

a999.pep Not found yet

The foregoing examples are intended to illustrate but not to limit the invention.

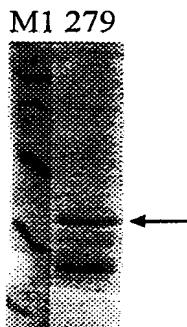
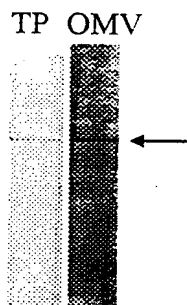
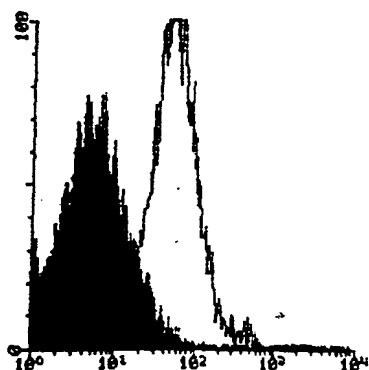
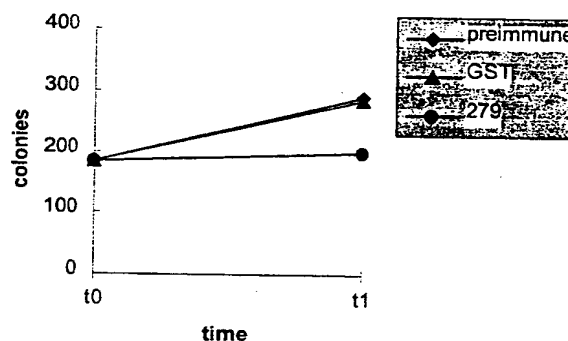
CLAIMS

1. A protein comprising a fragment of an amino acid sequence from SEQ ID 2790 wherein said fragment comprises at least 7 amino acids from said sequence.
2. A protein comprising an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020.
3. A protein having 50% or greater homology to a protein according to claim 1.
4. A protein comprising a fragment of an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020, wherein said fragment comprises 7 or more consecutive amino acids from said sequence.
5. An antibody which binds to a protein according to any one of claims 1 to 3.
6. A nucleic acid molecule which encodes a protein according to any one of claims 1 to 3.
7. A nucleic acid molecule according to claim 5, comprising a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019.
8. A nucleic acid molecule comprising a fragment of a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019, wherein said fragment comprises 10 or more consecutive nucleotides from said sequence.
9. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 5.
10. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 6.
11. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 7.
12. A composition comprising a protein, a nucleic acid molecule, or an antibody according to any preceding claim.
13. A composition according to claim 11 being a vaccine composition or a diagnostic composition.
14. A composition according to claim 11 for use as a pharmaceutical.
15. The use of a composition according to claim 11 in the manufacture of a medicament for the treatment or prevention of infection due to Neisserial bacteria.

16. A composition comprising a protein of claim 1 wherein said composition is immunogenic.

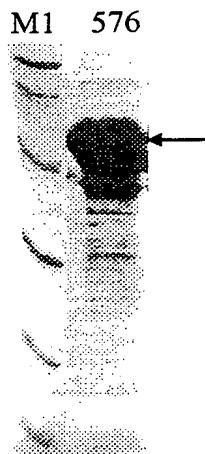
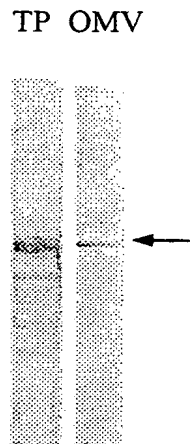
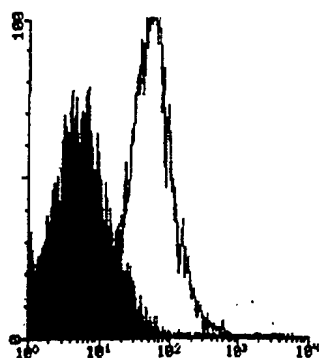
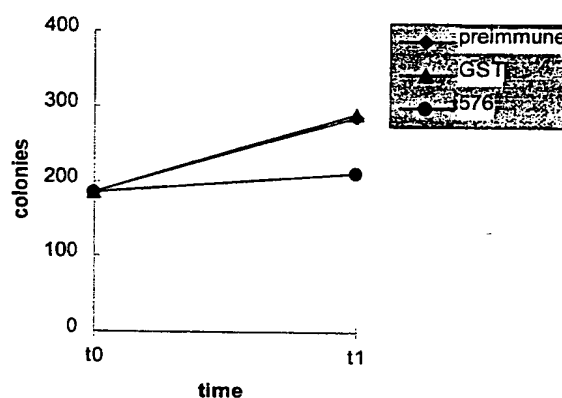
17. A composition comprising a protein of claim 2 wherein said composition is immunogenic.

18. A composition comprising a protein of claim 3 wherein said composition is immunogenic.

279 (10.5 kDa)**Fig. 2****A) PURIFICATION****B) WESTERN BLOT****C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****279**

The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that protein 279 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

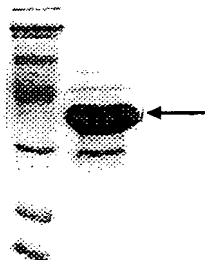
Fig. 3

576 (27.8 kDa)**A) PURIFICATION****B) WESTERN BLOT****C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****576**

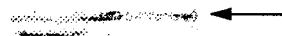
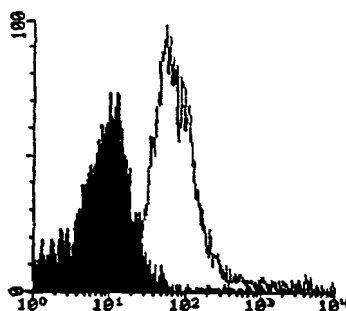
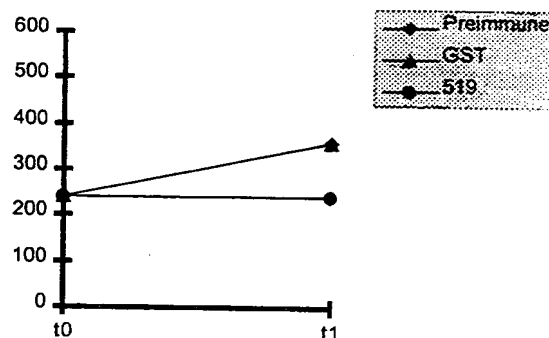
The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 576 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

519 (33 kDa)**Fig. 4****A) PURIFICATION**

M1 519

**B) WESTERN BLOT**

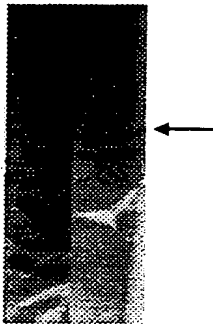
TP OMV

**C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****519**

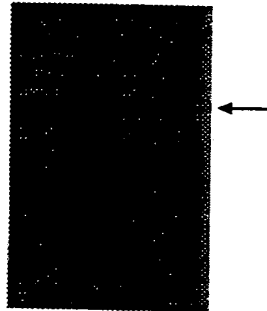
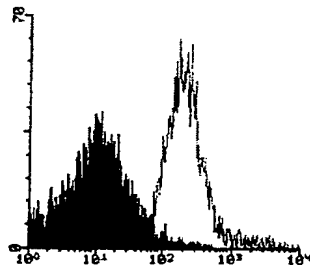
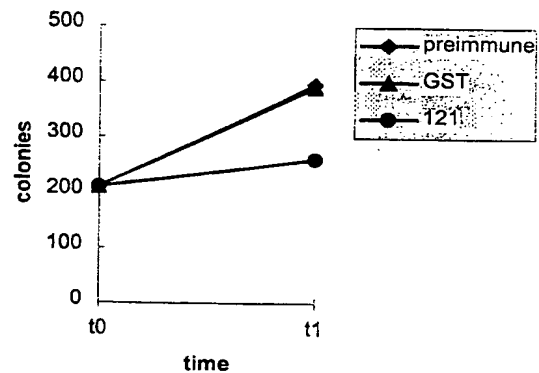
The predicted gene 519 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 519 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

121 (40 kDa)**A) PURIFICATION**

M1 121

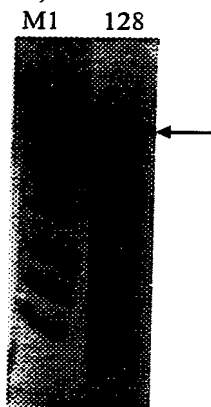
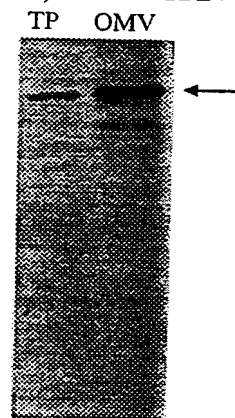
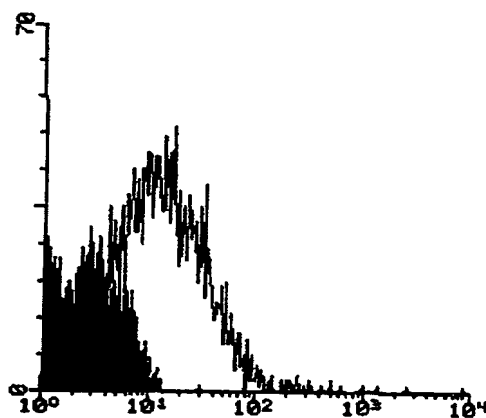
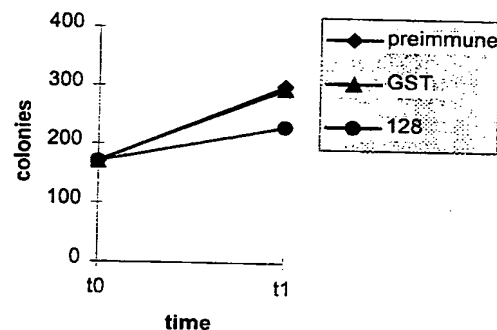
**B) WESTERN BLOT**

TP OMV

**C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****121**

The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

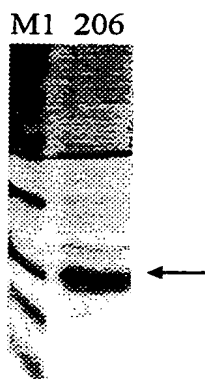
Fig. 5

128 (101 kDa)**Fig. 6****A) PURIFICATION****B) WESTERN BLOT****C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****128**

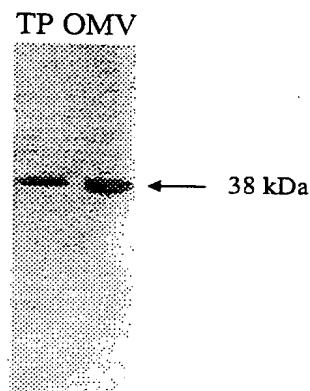
The predicted gene *128* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 7

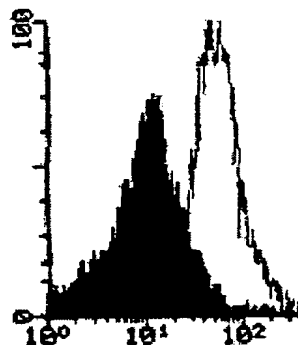
A) PURIFICATION



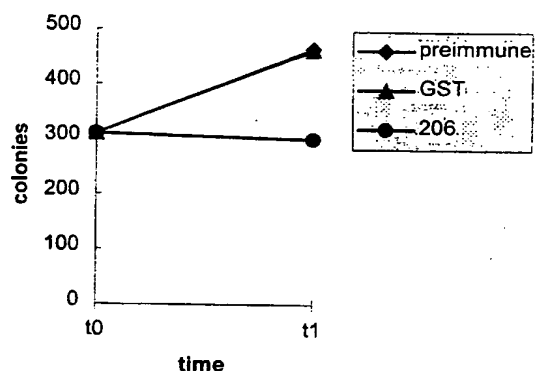
B) WESTERN BLOT



C) FACS



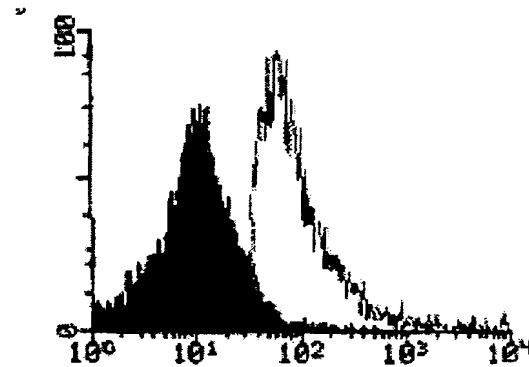
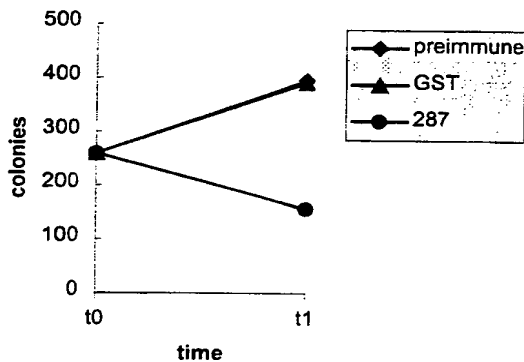
D) BACTERICIDAL ASSAY



E) ELISA assay: positive

206

The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worth noting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a reactive band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C is shown the FACS analysis, in panel D the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

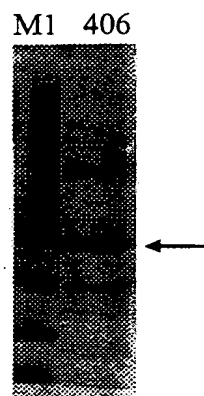
287 (78 kDa)**Fig. 8****A) PURIFICATION****B) FACS****C) BACTERICIDAL ASSAY****D) ELISA assay : positive****287**

The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A).

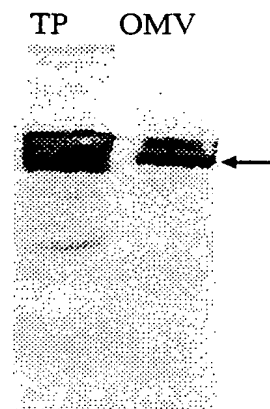
406 (33 kDa)

Fig. 9

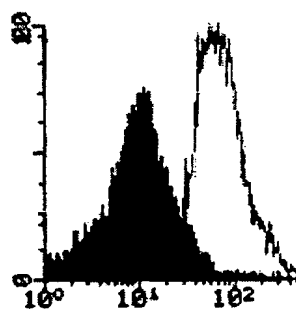
A) PURIFICATION



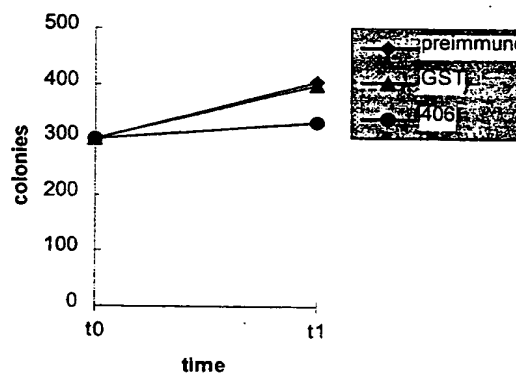
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY

E) ELISA assay : positive

406

The predicted gene 406 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

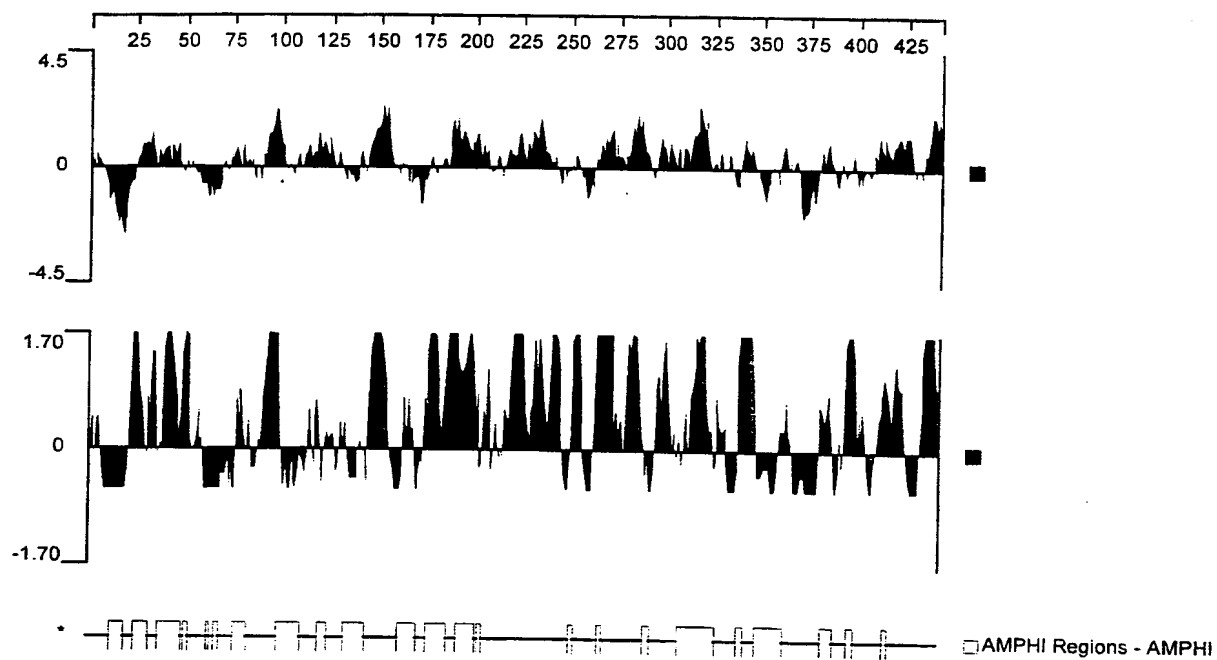
919Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 10

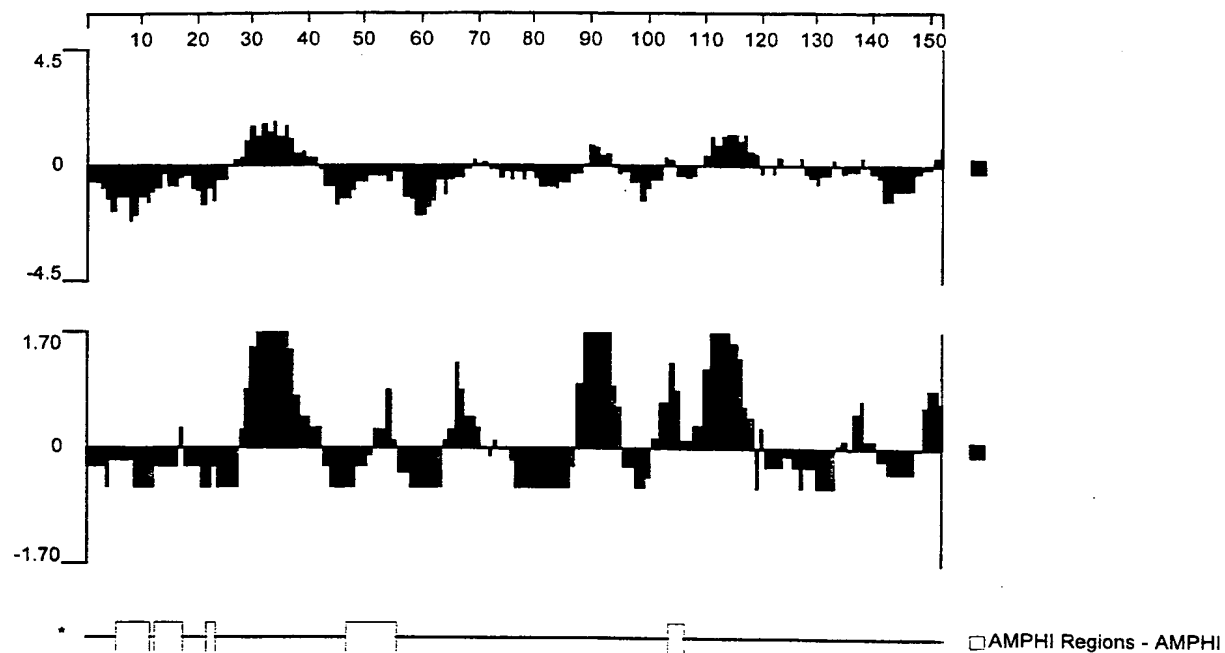
279Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 11

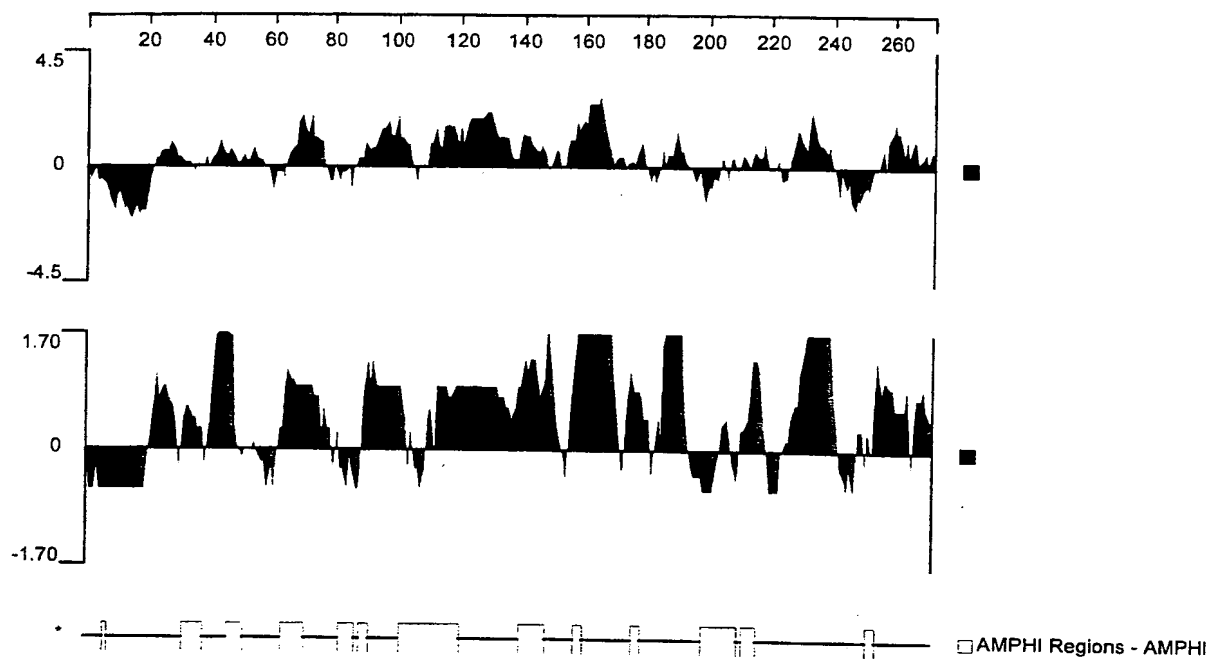
576-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 12

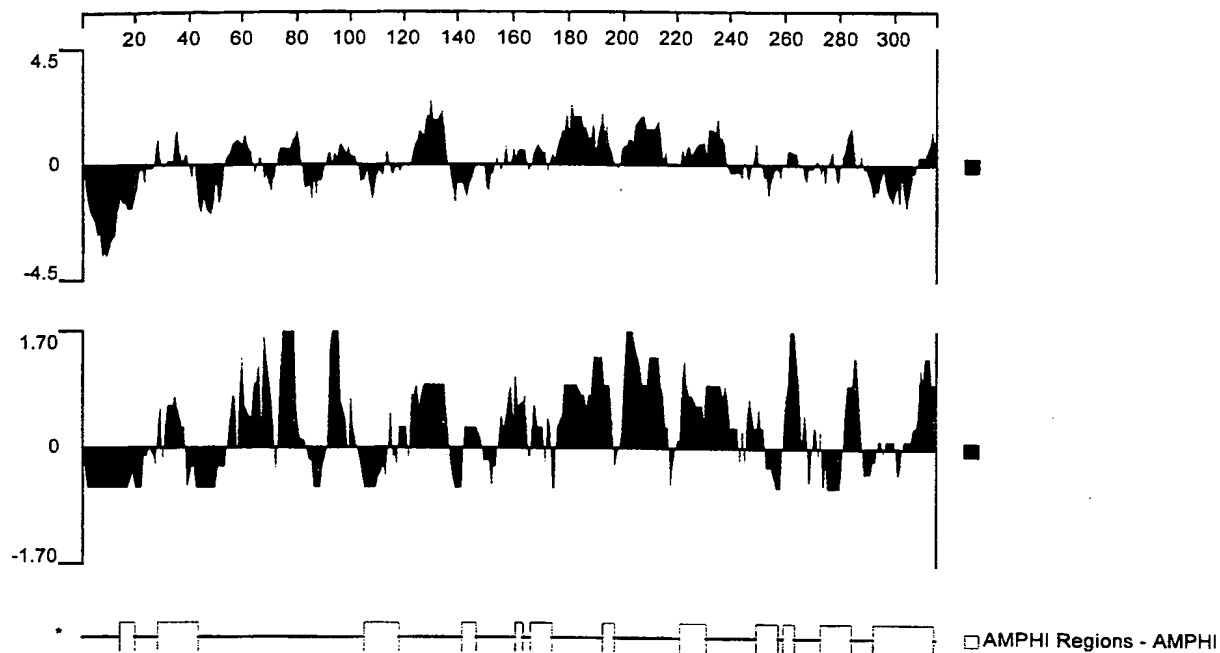
519-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 13

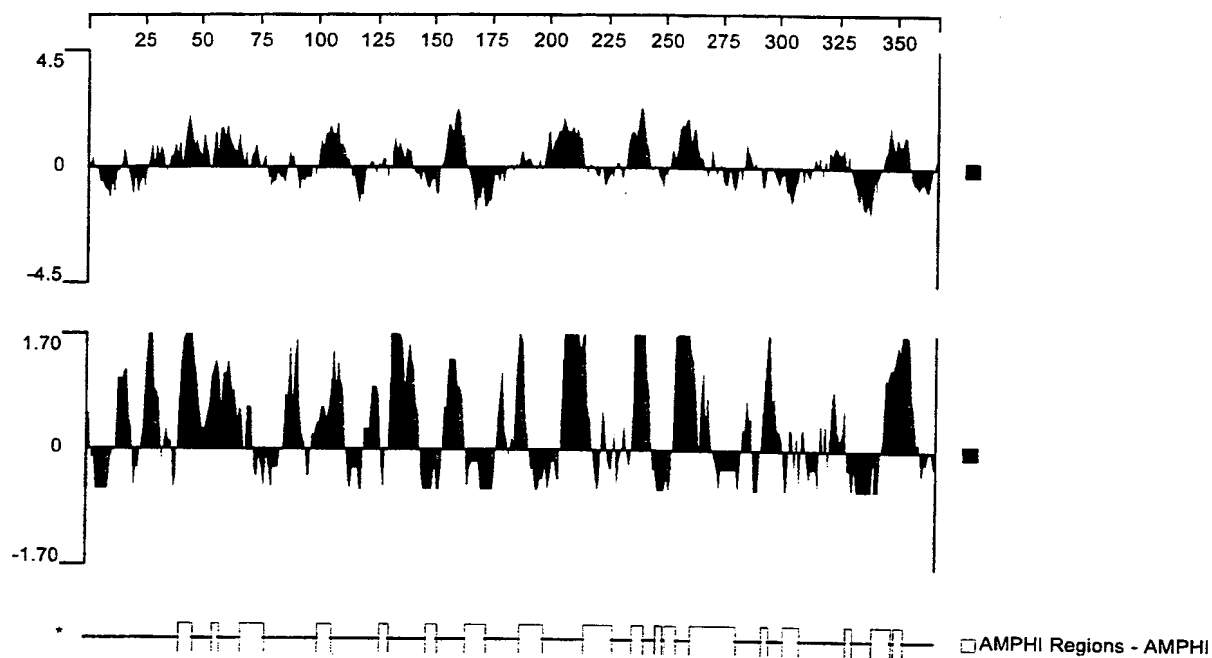
121-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 14

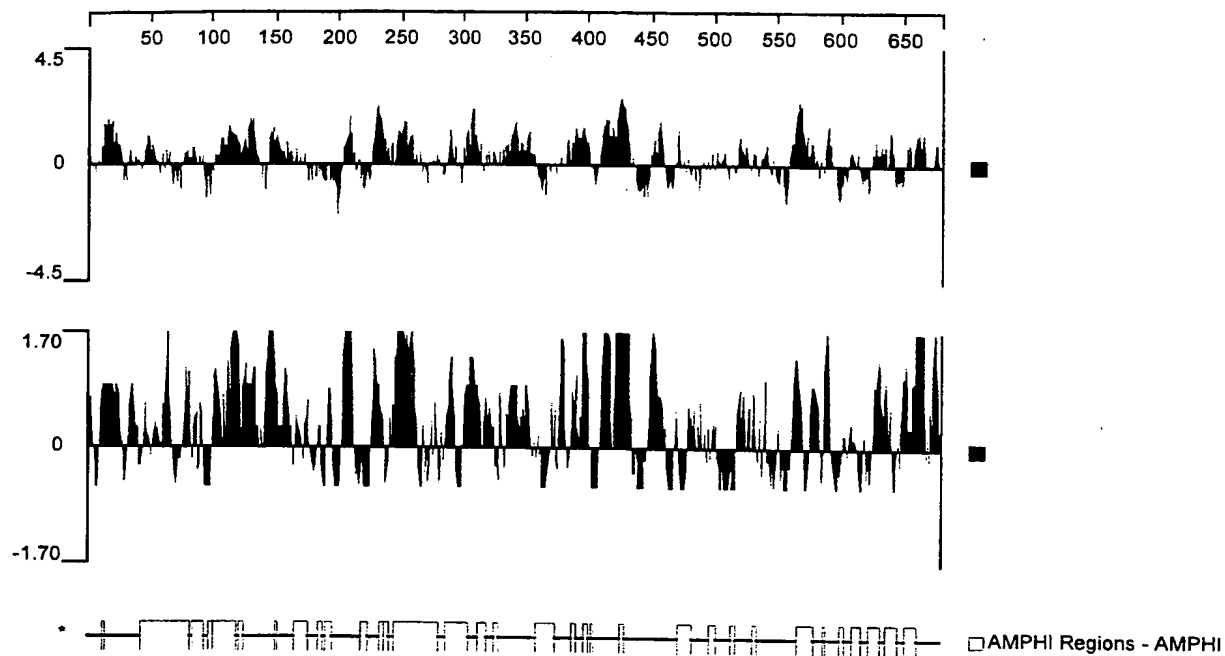
128-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 15

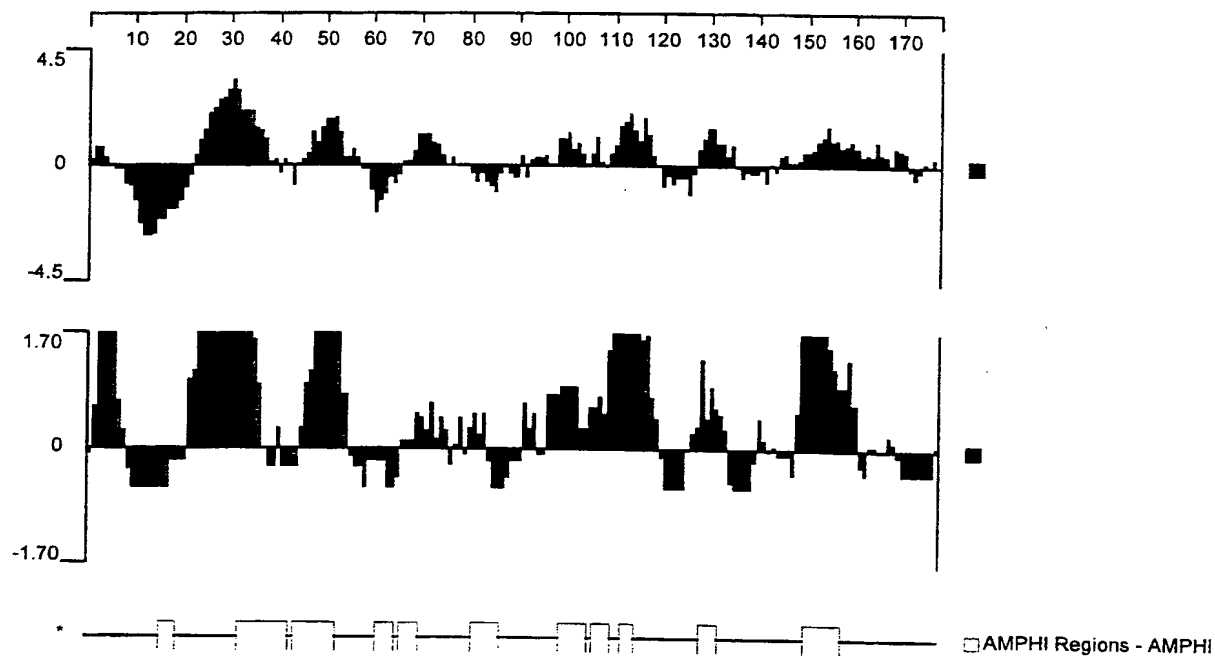
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 16

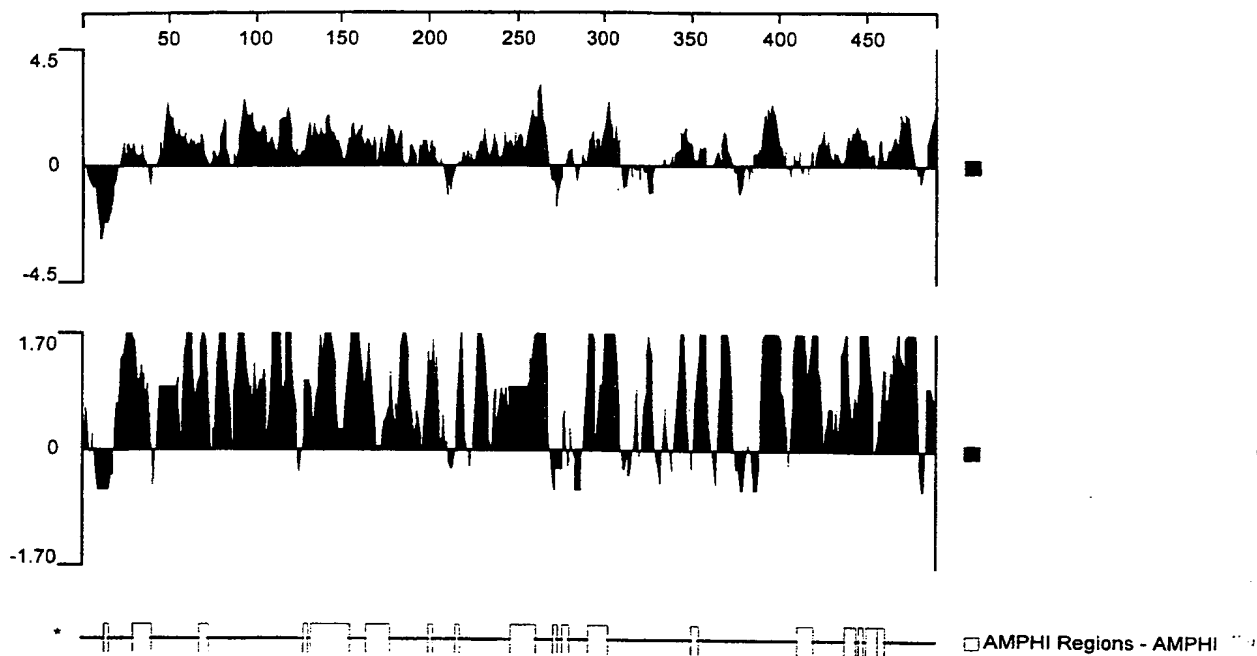
287Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 17

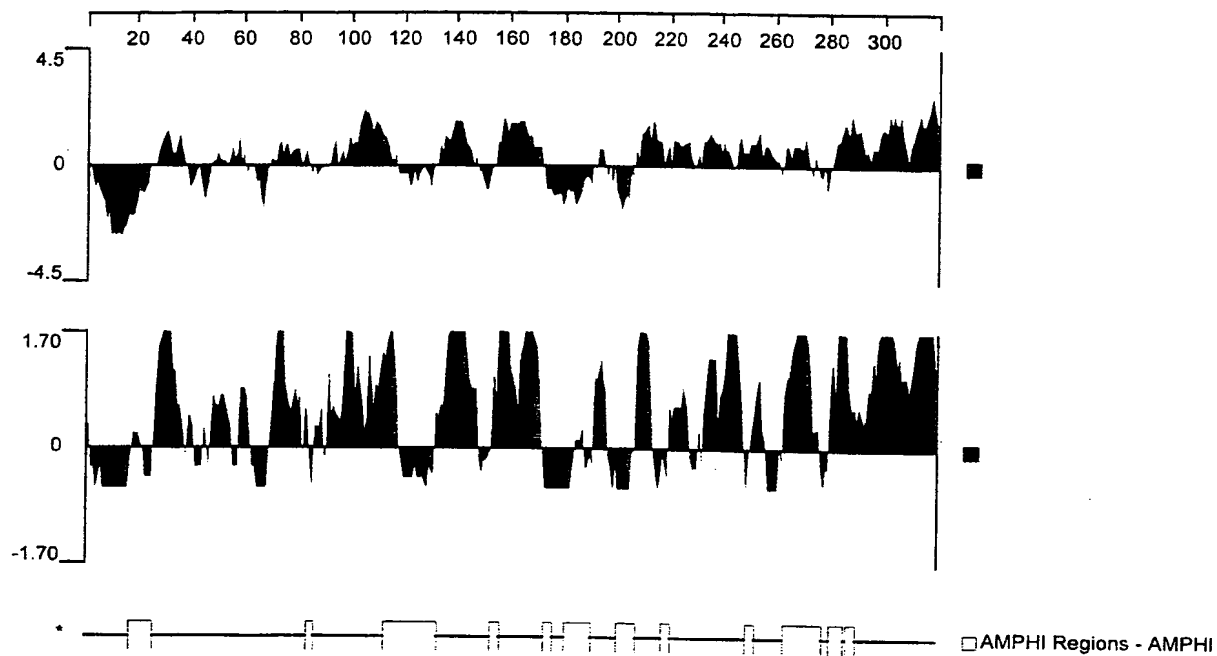
406Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 18

zo05_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo08_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
z2491	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo11_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo20_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo01_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo09_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo12_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo22_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo23_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo24_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo25_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo26_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo96_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo02_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo04_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo06_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo07_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo10_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo14_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo16_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo17_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo18_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo19_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo21_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo27_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo28_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo29_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo13_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo03_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo15_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
fa1090	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo32_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo33_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo05_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
zo08_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
z2491	61	NADELIGSAMGLNEQPVLVPVNRVPARRAGNADELIGNAMGLNEQPVLVPVNRVPARRAGNA
zo11_225	61	NADELIGSAMGLNEQPVLVPVNRVPARRAGNADELIGNAMGLNEQPVLVPVNRVPARRAGNA
zo20_225	61	NADELIGSAMGLNEQPVLVPVNRVPARRAGNADELIGNAMGLNEQPVLVPVNRVPARRAGNA
zo01_225	61	NADELIGSAMGLNEQPVLVPINRAPARRAGNADELIGSAMGLNEQPVLVPVNRVPARRAGNA
zo09_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
zo12_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
zo22_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
zo23_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
zo24_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
zo25_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
zo26_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
zo96_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
zo02_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
zo04_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
zo06_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
zo07_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
zo10_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
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zo16_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
zo17_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
zo18_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
zo19_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
zo21_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
zo27_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
zo28_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
zo29_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
zo13_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
zo03_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
zo15_225	61	NADELIGSAMGLNE.....QPVLVPVNRVPARRAGNA
fa1090	61	NADELIGSAMGLNE.....
zo32_225	61	NADELIGSAMGLNE.....
zo33_225	61	NADELIGSAMGLNE.....

Fig. 19A

Fig. 19B

zo05_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo08_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
z2491	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo11_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo20_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo01_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo09_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo12_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo22_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo23_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo24_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
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zo26_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo96_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo02_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo04_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo06_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
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zo14_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo16_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo17_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo18_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo19_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo21_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo27_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo28_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo29_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo13_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo03_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo15_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
fa1090	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo32_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo33_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*

Fig. 19C

gnmzq09 121 YQILDSVTTVSAKARLVDSRNGKVLWSGSASIREGSNNNSNSGLLGALVS AVVNQIANSLT
gnmzq31 121 YQILDSVTTVSAKARLVDSRNGKVLWSGSASIREGSNNNSNSGLLGALV GAVVNQIANSLT
fal090 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNSGLLGALV GAVVNQIANSLT
gnmzq32 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNSGLLGALV GAVVNQIANSLT
gnmzq33 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNSGLLGALV GAVVNQIANSLT
gnmzq01 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNSGLLGALV GAVVNQIANSLT
gnmzq05 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNSGLLGALV SAVVNQIANSLT
gnmzq08 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNSGLLGALV SAVVNQIANSLT
gnmzq02 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNSGLLGALV SAVVNQIANSLT
gnmzq03 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNSGLLGALV SAVVNQIANSLT
gnmzq04 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNSGLLGALV SAVVNQIANSLT
gnmzq07 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNSGLLGALV SAVVNQIANSLT
gnmzq10 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNSGLLGALV SAVVNQIANSLT
gnmzq11 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNSGLLGALV SAVVNQIANSLT
gnmzq13 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNSGLLGALV SAVVNQIANSLT
gnmzq15 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNSGLLGALV SAVVNQIANSLT
gnmzq16 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNSGLLGALV SAVVNQIANSLT
gnmzq17 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNSGLLGALV SAVVNQIANSLT
gnmzq19 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNSGLLGALV SAVVNQIANSLT
gnmzq21 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNSGLLGALV SAVVNQIANSLT
gnmzq22 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNSGLLGALV SAVVNQIANSLT
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gnmzq29 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNSGLLGALV SAVVNQIANSLT
z2491 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNSGLLGALV SAVVNQIANSLT
gnmzq14 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNSGLLGALV SAVVNQIANSLT
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gnmzq26 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNSGLLGALV SAVVNQIANSLT

gnmzq09 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq31 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
fal090 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq32 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq33 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq01 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq05 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq08 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq02 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq03 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq04 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq07 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq10 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq11 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq13 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
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gnmzq23 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
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gnmzq28 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq29 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
z2491 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq14 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq18 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq26 181 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

Fig. 20B

287_14 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVV...E.....KETE
287_2 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVV...E.....KETE
287_21 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVV...E.....KETE
z2491 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVV...E.....KETE
287_9 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVV...E.....KETE
fa1090 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVV...E.....KETE

287_14 50 KEDAPQAGSQGGGAPSAQGGQDMAAVSEENTGNGGAATDKPKNEDEGAQNDMPQNAADT
287_2 50 KEDAPQAGSQGGGAPSAQGGQDMAAVSEENTGNGGAATDKPKNEDEGAQNDMPQNAADT
287_21 50 KEDAPQAGSQGGGAPSAQGGQDMAAVSEENTGNGGAATDKPKNEDEGAQNDMPQNAADT
z2491 50 KEDAPQAGSQGGGAPSAQGGQDMAAVSEENTGNGGAATDKPKNEDEGAQNDMPQNAADT
287_9 61 VSGAPQADT...ODATAGKGGQDMAAVSEENTGNGGAATDKPKNEDEGAQNDMPQNAADT
fa1090 61 AGGAPQADT...ODATAGKGGQDMAAVSEENTGNGGAATDKPKNEDEGAQNDMPQNAADT

287_14 110 DSLTPNHPTASNMFPAGNMENQAPDAGESEOPANQPDMANADGMQGGDDPSAGGENAGNTA
287_2 110 DSLTPNHPTASNMFPAGNMENQAPDAGESEOPANQPDMANADGMQGGDDPSAGGENAGNTA
287_21 110 DSLTPNHPTASNMFPAGNMENQAPDAGESEOPANQPDMANADGMQGGDDPSAGGENAGNTA
z2491 110 DSLTPNHPTASNMFPAGNMENQAPDAGESEOPANQPDMANADGMQGGDDPSAGGENAGNTA
287_9 119 DSLTPNHPTASNMFPTRDMGNQAPDAGESEOPANQPDMANADGMQGGDDPSAGGENAGNTA
fa1090 117GENAGNTA

287_14 170 AOSTNOAENNOTAGSQNPASSTNPSATNSGGDEGRNTNNSV...IDGPSQNTLTHCKGDS
287_2 170 AOSTNOAENNOTAGSQNPASSTNPSATNSGGDEGRNTNNSV...IDGPSQNTLTHCKGDS
287_21 170 AOSTNOAENNOTAGSQNPASSTNPSATNSGGDEGRNTNNSV...IDGPSQNTLTHCKGDS
z2491 170 AOSTNOAENNOTAGSQNPASSTNPSATNSGGDEGRNTNNSV...IDGPSQNTLTHCKGDS
287_9 178 DOSTNOAENNOTAGSQNPASSTNPSATNSGGDEGRNTNNSV...IDGPSQNTLTHCKGDS
fa1090 117 .ESANTGNNQAGSSDSAPASNPAPANGGSDGGRNTNNSV...IDGPSQNTLTHCKGDS

287_14 230 CSGNNFLDEEVQIKSEFEKLSDAKISNYKKDGKNDGKNDK...FVGLVADSVQMKGINQYII
287_2 230 CSGNNFLDEEVQIKSEFEKLSDAKISNYKKDGKNDGKNDK...FVGLVADSVQMKGINQYII
287_21 230 CSGNNFLDEEVQIKSEFEKLSDAKISNYKKDGKNDGKNDK...FVGLVADSVQMKGINQYII
z2491 230 CSGNNFLDEEVQIKSEFEKLSDAKISNYKKDGKNDGKNDK...FVGLVADSVQMKGINQYII
287_9 238 CDRD...FLDEEAPPKSEFEKLSDAKISNYKKDGKNDGKNDK...FVGLVADSVQMKGINQYII
fa1090 176 CNGDNFLDEEAPPKSEFEKLSDAKISNYKKDGKNDGKNDK...FVGLVADSVQMKGINQYII

287_14 290 FYKPKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
287_2 290 FYKPKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
287_21 286 FYKPKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
z2491 286 FYKPKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
287_9 293 IYKDKSAS...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
fa1090 232 FYTDKPT...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG

287_14 348 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPS...GRFAA
287_2 348 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPS...GRFAA
287_21 344 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPS...GRFAA
z2491 344 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPS...GRFAA
287_9 353 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPS...GRFAA
fa1090 285 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPS...GRFAA

287_14 408 KVDGSGSKSVDGIIDSGDGLHMGTOQKFKAAIDGNGFKGTWTENGCGDVSG...FYGPAGEEVA
287_2 408 KVDGSGSKSVDGIIDSGDGLHMGTOQKFKAAIDGNGFKGTWTENGCGDVSG...FYGPAGEEVA
287_21 404 KVDGSGSKSVDGIIDSGDGLHMGTOQKFKAAIDGNGFKGTWTENGCGDVSG...FYGPAGEEVA
z2491 404 KVDGSGSKSVDGIIDSGDGLHMGTOQKFKAAIDGNGFKGTWTENGCGDVSG...FYGPAGEEVA
287_9 413 KVDGSGSKSVDGIIDSGDGLHMGTOQKFKAAIDGNGFKGTWTENGCGDVSG...FYGPAGEEVA
fa1090 345 KVDGSGSKSVDGIIDSGDGLHMGTOQKFKAAIDGNGFKGTWTENGCGDVSG...FYGPAGEEVA

FIG. 21A

287_14	468	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_2	468	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_21	464	GKYSYRPTDAEKGGFGVFAGKKEQD*
z2491	464	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_9	473	GKYSYRPTDAEKGGFGVFAGKKEQD*
fa1090	405	GKYSYRPTDAEKGGFGVFAGKKTRD*

FIG. 21B

z2491_519 1 MEFFFIILLAAVAVFVFGKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
zv26_519 1 MEFFFIILLAAVAVFVFGKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
zv22_519ass 1 MEFFFIILLAAVAVFVFGKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
fa1090_519 1 MEFFFIILLAAVAVFVFGKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
zv32_519 1 MEFFFIILLAAVAVFVFGKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
zv11_519 1 MEFFFIILLAAVAVFVFGKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
zv28_519 1 MEFFFIILLAAVAVFVFGKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
zv96_519 1 MEFFFIILLAAVAVFVFGKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
zv02_519 1 MEFFFIILLAAVAVFVFGKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
zv03_519 1 MEFFFIILLAAVAVFVFGKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
zv04_519 1 MEFFFIILLAAVAVFVFGKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
zv05_519 1 MEFFFIILLAAVAVFVFGKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
zv01_519 1 MEFFFIILLAAVAVFVFGKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
zv07_519 1 MEFFFIILLAAVAVFVFGKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
zv12_519 1 MEFFFIILLAAVAVFVFGKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
zv18_519 1 MEFFFIILLAAVAVFVFGKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
zv19_519 1 MEFFFIILLAAVAVFVFGKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
zv21_519ass 1 MEFFFIILLAAVAVFVFGKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
zv27_519 1 MEFFFIILLAAVAVFVFGKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
zv20_519ass 1 MEFFFIILLAAVAVFVFGKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
zv06_519ass 1 MEFFFIILLAAVAVFVFGKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
zv29_519ass 1 MEFFFIILLAAVAVFVFGKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL

z2491_519 61 KEIPLDVP SQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv26_519 61 KEIPLDVP SQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv22_519ass 61 KEIPLDVP SQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
fa1090_519 61 KEIPLDVP SQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv32_519 61 KEIPLDVP SQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv11_519 61 KEIPLDVP SQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv28_519 61 KEIPLDVP SQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv96_519 61 KEIPLDVP SQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv02_519 61 KEIPLDVP SQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv03_519 61 KEIPLDVP SQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv04_519 61 KEIPLDVP SQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv05_519 61 KEIPLDVP SQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv01_519 61 KEIPLDVP SQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv07_519 61 KEIPLDVP SQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv12_519 61 KEIPLDVP SQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv18_519 61 KEIPLDVP SQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv19_519 61 KEIPLDVP SQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv21_519ass 61 KEIPLDVP SQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv27_519 61 KEIPLDVP SQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv20_519ass 61 KEIPLDVP SQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv06_519ass 61 KEIPLDVP SQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv29_519ass 61 KEIPLDVP SQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG

z2491_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv26_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv22_519ass 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
fa1090_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv32_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv11_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv28_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv96_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv02_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv03_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv04_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv05_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv01_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv07_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv12_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv18_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv19_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv21_519ass 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv27_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv20_519ass 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv06_519ass 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv29_519ass 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE

FIG. 22A

z2491_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv26_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv22_519ass	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
fa1090_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv32_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv11_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv28_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv96_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv02_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv03_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv04_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv05_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv01_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv07_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv12_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv18_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv19_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv21_519ass	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv27_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv20_519ass	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv06_519ass	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv29_519ass	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR

z2491_519	241	LVAEANAETIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv26_519	241	LVAEANAETIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv22_519ass	241	LVAEANAETIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
fa1090_519	241	LVAEANAETIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv32_519	241	LVAEANAETIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv11_519	241	LVAEANAETIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv28_519	241	LVAEANAETIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv96_519	241	LVAEANAETIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv02_519	241	LVAEANAETIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv03_519	241	LVAEANAETIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv04_519	241	LVAEANAETIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv05_519	241	LVAEANAETIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv01_519	241	LVAEANAETIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv07_519	241	LVAEANAETIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv12_519	241	LVAEANAETIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv18_519	241	LVAEANAETIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv19_519	241	LVAEANAETIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv21_519ass	241	LVAEANAETIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv27_519	241	LVAEANAETIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv20_519ass	241	LVAEANAETIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv06_519ass	241	LVAEANAETIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv29_519ass	241	LVAEANAETIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL

z2491_519	301	ISAGMKIIDSSKTAK*
zv26_519	301	ISAGMKIIDSSKTAK*
zv22_519ass	301	ISAGMKIIDSSKTAK*
fa1090_519	301	ISAGMKIIDSSKTAK*
zv32_519	301	ISAGMKIIDSSKTAK*
zv11_519	301	ISAGMKIIDSSKTAK*
zv28_519	301	ISAGMKIIDSSKTAK*
zv96_519	301	ISAGMKIIDSSKTAK*
zv02_519	301	ISAGMKIIDSSKTAK*
zv03_519	301	ISAGMKIIDSSKTAK*
zv04_519	301	ISAGMKIIDSSKTAK*
zv05_519	301	ISAGMKIIDSSKTAK*
zv01_519	301	ISAGMKIIDSSKTAK*
zv07_519	301	ISAGMKIIDSSKTAK*
zv12_519	301	ISAGMKIIDSSKTAK*
zv18_519	301	ISAGMKIIDSSKTAK*
zv19_519	301	ISAGMKIIDSSKTAK*
zv21_519ass	301	ISAGMKIIDSSKTAK*
zv27_519	301	ISAGMKIIDSSKTAK*
zv20_519ass	301	ISAGMKIIDSSKTAK*
zv06_519ass	301	ISAGMKIIDSSKTAK*
zv29_519ass	301	ISAGMKIIDSSKTAK*

Fig. 22B

fa1090	361	IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm33asbc	361	IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm32asbc	361	IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm23asbc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm27bc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm09	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm10	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm24	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm25	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm14	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm04	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm11asbc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm08n	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm96	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm01	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm02	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm03	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm07	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm12	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm18	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm19	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm20	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm21	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm06	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm17	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm13	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm05	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
z2491	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm22	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm26	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm28	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm29asbc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm16	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm15	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm31asbc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK

fa1090	421	QKTTGYVWQLLPNGMKPEYRP*
zm33asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm32asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm23asbc	421	MKEPGYVWQLLPNGMKPEYRP*
zm27bc	421	MKEPGYVWQLLPNGMKPEYRP*
zm09	421	QKTTGYVWQLLPNGMKPEYRP*
zm10	421	QKTTGYVWQLLPNGMKPEYRP*
zm24	421	QKTTGYVWQLLPNGMKPEYRP*
zm25	421	QKTTGYVWQLLPNGMKPEYRP*
zm14	421	QKTTGYVWQLLPNGMKPEYRP*
zm04	421	QKTTGYVWQLLPNGMKPEYRP*
zm11asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm08n	421	QKTTGYVWQLLPNGMKPEYRP*
zm96	421	QKTTGYVWQLLPNGMKPEYRP*
zm01	421	QKTTGYVWQLLPNGMKPEYRP*
zm02	421	QKTTGYVWQLLPNGMKPEYRP*
zm03	421	QKTTGYVWQLLPNGMKPEYRP*
zm07	421	QKTTGYVWQLLPNGMKPEYRP*
zm12	421	QKTTGYVWQLLPNGMKPEYRP*
zm18	421	QKTTGYVWQLLPNGMKPEYRP*
zm19	421	QKTTGYVWQLLPNGMKPEYRP*
zm20	421	QKTTGYVWQLLPNGMKPEYRP*
zm21	421	QKTTGYVWQLLPNGMKPEYRP*
zm06	421	QKTTGYVWQLLPNGMKPEYRP*
zm17	421	QKTTGYVWQLLPNGMKPEYRP*
zm13	421	QKTTGYVWQLLPNGMKPEYRP*
zm05	421	QKTTGYVWQLLPNGMKPEYRP*
z2491	421	QKTTGYVWQLLPNGMKPEYRP*
zm22	421	QKTTGYVWQLLPNGMKPEYRP*
zm26	421	QKTTGYVWQLLPNGMKPEYRP*
zm28	421	QKTTGYVWQLLPNGMKPEYRP*
zm29asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm16	421	QKTTGYVWQLLPNGMKPEYRP*
zm15	421	QKTTGYVWQLLPNGMKPEYRP*
zm31asbc	421	QKTTGYVWQLLPNGMKPEYRP*

Fig. 23D



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/31, C07K 14/22, 16/12, C12Q 1/68, A61K 39/095, G01N 33/50		A3	(11) International Publication Number: WO 99/57280
(21) International Application Number: PCT/US99/09346		(43) International Publication Date: 11 November 1999 (11.11.99)	
(22) International Filing Date: 30 April 1999 (30.04.99)		(US). MASIGNANI, Vega [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). MORA, Marirosa [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). PETERSEN, Jeremy [US/US]; Arlington, VA (US). PIZZA, Mariagratia [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). RAPPUOLI, Rino [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). RATTI, Giulio [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). SCALATO, Enzo [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). SCARSELLI, Maria [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). TETTELIN, Herve [US/US]; Gaithersburg, MD (US). VENTER, J., Craig [US/US]; Rockville, MD (US).	
(30) Priority Data:			
60/083,758 1 May 1998 (01.05.98) US 60/094,869 31 July 1998 (31.07.98) US 60/098,994 2 September 1998 (02.09.98) US 60/099,062 2 September 1998 (02.09.98) US 60/103,749 9 October 1998 (09.10.98) US 60/103,794 9 October 1998 (09.10.98) US 60/103,796 9 October 1998 (09.10.98) US 60/121,528 25 February 1999 (25.02.99) US		(74) Agent: HARBIN, Alisa, A.; Chiron Corporation, Intellectual Property - R440, P.O. Box 8097, Emeryville, CA 94662-8097 (US).	
(71) Applicants (for all designated States except US): CHIRON CORPORATION [US/US]; 4560 Horton Street, Emeryville, CA 94608 (US). THE INSTITUTE FOR GENOMIC RESEARCH [US/US]; 9212 Medical Center Drive, Rockville, MD 20850 (US).			
(72) Inventors; and		(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).	
(75) Inventors/Applicants (for US only): FRASER, Claire [US/US]; Rockville, MD (US). GALEOTTI, Cesira [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). GRANDI, Guido [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). HICKEY, Erin [US/US]; Gaithersburg, MD			
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(54) Title: NEISSERIA MENINGITIDIS ANTIGENS AND COMPOSITIONS

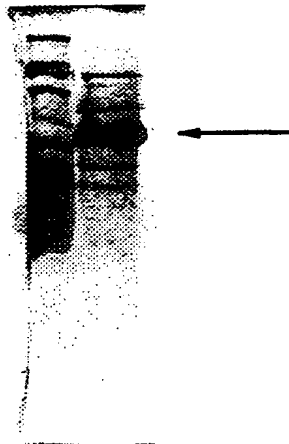
(57) Abstract

The invention provides proteins from Neisseria meningitidis, including the amino acid sequences and the corresponding nucleotide sequences. The proteins are predicted to be useful antigens for vaccines and/or diagnostics.

919 (46 kDa)

PURIFICATION

M1 919



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INTERNATIONAL SEARCH REPORT

International Application No
PCT/ES 99/09346

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/31 C07K14/22 C07K16/12 C12Q1/68 A61K39/095
G01N33/50

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K C12Q A61K G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE TREMBL [Online] EMBL ID Q55666, AC Q55666, 1 November 1996 (1996-11-01) TABATA S: "Membrane-bound lytic transglycosylase A MltA Synechocystis sp. strain PCC 6803" XP002130156 Note: 100% aa seq identity of aa 342-350 with aa 392-400 of SEQ ID NOs 2790 and 2792, 27.6% (26.9%) aa seq identity with SEQ ID NO:2790 (2792) in 370 (387) aa overlap. the whole document --- -/-	1,4-6,9, 12

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

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Date of the actual completion of the international search

26 May 2000

Date of mailing of the international search report

15.06.00

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

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van de Kamp, M

INTERNATIONAL SEARCH REPORT

International Application No

PL./US 99/09346

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EP 0 818 465 A (BIOLOG MOLECULAIRE DES PLANTES ; INST OF MOLECULAR BIOTECHNOLOG (DE) 14 January 1998 (1998-01-14) Note: 100% nt seq identity of nt 367951-367961 of SEQ ID NO:1 with nt 163-173 of SEQ ID NO:2789. page 108	8,11,12
A	--- LOMMATZSCH J ET AL.: "Outer membrane localization of murein hydrolases: MltA, a third lipoprotein lytic transglycosylase in Escherichia coli" JOURNAL OF BACTERIOLOGY, vol. 179, no. 17, September 1997 (1997-09), pages 5465-5470, XP002130154 Note: 33.7% (35.7%) aa seq identity with SEQ ID NO:2790 (2792) in 273 (207) aa overlap. abstract	1-12
A	--- DILLARD J P ET AL.: "A peptidoglycan hydrolase similar to bacteriophage endolysins acts as an autolysin in Neisseria gonorrhoeae" MOLECULAR MICROBIOLOGY, vol. 25, no. 5, September 1997 (1997-09), pages 893-901, XP000878964 abstract	1-12
A	--- WO 96 29412 A (IAF BIO VAC INC ; BRODEUR BERNARD R (CA); MARTIN DENIS (CA); HAMEL) 26 September 1996 (1996-09-26) cited in the application the whole document examples 1-12	1-18
A	--- WO 94 08013 A (OREGON STATE) 14 April 1994 (1994-04-14) the whole document examples 1-7	1-18
A	--- WO 92 13871 A (UNIV WASHINGTON) 20 August 1992 (1992-08-20) the whole document examples 1-10	1-18
A	--- BLAKE M S ET AL.: "Vaccines for gonorrhoea: where are we on the curve?" TRENDS IN MICROBIOLOGY, vol. 3, no. 12, December 1995 (1995-12), pages 469-474, XP000876514 the whole document --- -/--	1-18

INTERNATIONAL SEARCH REPORT

International Application No

PC 99/09346

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	POOLMAN J T: "Development of a meningococcal vaccine" INFECTIOUS AGENTS AND DISEASE, vol. 4, no. 1, March 1995 (1995-03), pages 13-28, XP000876540 the whole document ---	1-18
X	WO 96 01901 A (RHONE POULENC RORER SA ;BLANC VERONIQUE (FR); THIBAUT DENIS (FR);) 25 January 1996 (1996-01-25) Note: 100% nt seq ident of bp 170-156 of SEQ ID NO:1 (rev DNA) with bp 202-216 of SEQ ID NO:1 (61.2% in 348 bp overlap), 40.7% seq ident of transl SEQ ID NO:1 with SEQ ID NO:2 in 118 aa overlap. page 102-104 example 1 ---	8,11,12
X	WO 97 37044 A (ASTRA AB ;ALM RICHARD A (US); SMITH DOUGLAS (US)) 9 October 1997 (1997-10-09) Note: 100% aa seq identity of aa 204-211, 186-193 & 352-359 of transl SEQ ID NOs 227, 345 & 1003, resp., with aa 59-66 of SEQ ID NO:2, 37.4% aa seq identity with SEQ ID NO:2 in 115 aa overlap. page 268-269 page 344 page 909-910 page 23, paragraph B.4 ---	4,12-14
X	DATABASE SWISSPROT [Online] ID YPCP YEREN, AC P31485, 1 July 1993 (1993-07-01) BAEUMLER A J ET AL.: "Hypothetical 29.6 kD protein in PCP 5' region (ORF1)" XP002138650 Note: 100% aa seq identity of aa 148-159 with aa 140-151 of SEQ ID NO:442, 43.4% aa seq identity with SEQ ID NO:442 in 256 aa overlap. the whole document ---	4,12
A	-& BAUMLER A J ET AL.: "A lipoprotein of Yersinia enterocolitica facilitates ferrioxamine uptake in Escherichia coli" JOURNAL OF BACTERIOLOGY, vol. 174, no. 3, February 1992 (1992-02), pages 1029-1035, XP000907295 page 1031, left-hand column, line 11 -right-hand column, line 15 ---	4,12
	-/--	

INTERNATIONAL SEARCH REPORT

International Application No.

PL /US 99/09346

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE SWISSPROT [Online] ID YDHH_HAEIN, AC P44861, 1 November 1995 (1995-11-01) FLEISCHMANN R D ET AL.: "Hypothetical protein HI0753" XP002138651 Note: 100% aa seq identity of aa 143-156 with aa 140-153 of SEQ ID NO:442, 41.6% aa seq identity with SEQ ID NO:442 in 377 aa overlap. the whole document</p> <p>---</p>	4,12
X	<p>WO 96 33276 A (HUMAN GENOME SCIENCES INC ;UNIV JOHNS HOPKINS (US)) 24 October 1996 (1996-10-24) Note: 100% nt seq identity of bp 816794-816807 with bp 289-302 of SEQ ID NO:441 (54.3% in 484 bp overlap), 100% aa seq identity of translated sequence with SEQ ID NO:442 in 14 aa overlap. page 77.488 Note: 100% nt seq identity of bp 230516-230526 with bp 1501-1511 of SEQ ID NO:489 (57.4% in 1292 bp overlap), 100% aa seq identity of translated sequence with SEQ ID NO:490 in 13 aa overlap. page 77.139 page 76.37, line HI0215 Note: 100% nt seq identity of bp 1025409-1025418 with bp 1339-1330 (rev strand) of SEQ ID NO:1201 (72.0% in 50 bp overlap). page 77.612</p> <p>---</p>	4,8, 11-14
X	<p>CONLIN C A ET AL.: "Escherichia coli prlC encodes an endopeptidase and is homologous to the Salmonella typhimurium opdA gene" JOURNAL OF BACTERIOLOGY, vol. 174, no. 18, September 1992 (1992-09), pages 5881-5997, XP000907300 Note: 100% nt seq ident of bp 1824-1837 with bp 1480-1493 of SEQ ID NO:489 (59.7% in 1282 bp overlap), 100% aa seq ident of aa 495-507 with aa 492-504 of SEQ ID NO:490 (49.5% in 679 aa overlap). abstract figure 2</p> <p>---</p> <p>-/--</p>	4,8,11, 12

INTERNATIONAL SEARCH REPORT

International Application No.

PCT/US 99/09346

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE SWISSPROT [Online] ID OPDA HAEIN, AC P44573, 1 November 1995 (1995-11-01) FLEISCHMANN R D ET AL.: "Oligopeptidase A (EC 3.4.24.70)" XP002138652 Note: 100% aa seq identity of aa 496-508 with aa 492-504 of SEQ ID NO:490, 49.0% aa seq identity in 677 aa overlap. the whole document</p> <p>---</p>	4,12
X	<p>ROKBI B ET AL.: "Evaluation of recombinant transferrin - binding protein B variants from Neisseria meningitidis for their ability to induce cross-reactive and bactericidal antibodies against a genetically diverse collection of serogroup B strains." INFECTION AND IMMUNITY, vol. 65, no. 1, January 1997 (1997-01), pages 55-63, XP002138643 abstract</p> <p>---</p>	5
P,A	<p>DATABASE TREMBL [Online] EMBL ID 069750, AC 069750, 1 August 1998 (1998-08-01) ROKBI B ET AL.: "Transferrin binding protein B, TbpB, Neisseria meningitidis" XP002138653 Note: 22.3% aa seq identity with SEQ ID NO:1202 in 488 aa overlap. the whole document</p> <p>---</p>	4,8, 12-15,17
A	<p>-& ROKBI B ET AL.: "Heterogeneity of tbpB, the transferrin-binding protein B gene, among serogroup B Neisseria meningitidis strains of the ET-5 complex" CLINICAL AND DIAGNOSTIC LABORATORY IMMUNOLOGY, vol. 4, no. 5, September 1997 (1997-09), pages 522-529, XP002138644 abstract</p> <p>---</p> <p>-/--</p>	5,8, 12-15,17

INTERNATIONAL SEARCH REPORT

International Application No

PL./US 99/09346

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>DATABASE GCG GENESEQ [Online] ID W14640, AC W14640, 5 March 1998 (1998-03-05) QUENTIN-MILLET M J ET AL.: "N. meningitidis HTR Tbp2 (del3777-385, del407-465, del488-508)" XP002138654 Note: 23.5% aa seq identity with SEQ ID NO:1202 in 571 aa overlap. the whole document</p>	4,8, 12-15,17
A	<p>-& WO 97 13860 A (PASTEUR MERIEUX SERUMS VACC; QUENTIN MILLET MARIE JOSE (FR); ROKBI)) 17 April 1997 (1997-04-17) claim 11</p>	4,8, 12-15,17
X	<p>--- DATABASE EMPR01 [Online] EMBL ID AF034831, AC AF034831, 4 December 1997 (1997-12-04) YOU Z ET AL.: "Rhizobium etli stomatin like protein (slp) gene, complete cds." XP002138655 Note: 100% nt seq ident of bp 4384-4395 with bp 529-540 of SEQ ID NO:1455 (54.4% in 638 bp overlap), 100% aa seq ident of aa 1394-1403 with aa 109-118 of SEQ ID NO:1456 (41.2% in 182 aa overlap). the whole document</p>	4,8,11, 12
P,X	<p>-& YOU Z ET AL.: "A stomatin-like protein encoded by the slp gene of Rhizobium etli is required for nodulation competitiveness on the common bean" MICROBIOLOGY, vol. 144, no. 9, September 1998 (1998-09), pages 2619-2627, XP000907294 abstract figure 2</p>	4,8,11, 12
X	<p>--- HUANG M ET AL.: "A stomatin-like protein necessary for mechanosensation in C. elegans" NATURE, vol. 378, no. 6554, 16 November 1995 (1995-11-16), pages 292-295, XP002138646 Note: 100% aa seq identity of aa 233-239 with aa 110-117 of SEQ ID NO:1456, 29.9% aa seq identity in 234 aa overlap. abstract figure 1</p> <p>--- -/--</p>	4,12

INTERNATIONAL SEARCH REPORT

 International Application No
 PCT/US 99/09346

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>WONG C Y ET AL.: "Cloning and characterization of two immunophilin-like genes, ilpA and fkpA, on a single 3.9-kilobase fragment of Aeromonas hydrophila genomic DNA"</p> <p>JOURNAL OF BACTERIOLOGY, vol. 179, no. 11, June 1997 (1997-06), pages 3397-3403, XP002138647</p> <p>Note: 100% nt seq ident of bp 2659-2672 with bp 613-626 of SEQ ID NO:1745 (59.2% in 655 bp overlap), 100% aa seq ident of aa 205-216 with aa 200-211 of SEQ ID NO:1746 (44.9% in 265 aa overlap). abstract figure 2</p> <p style="text-align: center;">---</p>	4,8, 11-14
X	<p>DATABASE EMPRO2 [Online] EMBL ID NE01198, AC U001198, 23 November 1993 (1993-11-23)</p> <p>MCALLISTER C F ET AL.: "Neisseria elongata NRL FKBP immunophilin homolog gene"</p> <p>XP002138656</p> <p>Note: 100% nt seq identity of bp 125-138 with bp 635-648 of SEQ ID NO:1745 (65.8% nt seq identity in 237 bp overlap). the whole document</p>	8,11,12
X	<p>-& MCALLISTER C F ET AL.: "Analysis in Neisseria meningitidis and other Neisseria species homologous to the FKBP immunophilin family"</p> <p>MOLECULAR MICROBIOLOGY, vol. 10, no. 1, October 1993 (1993-10), pages 13-23, XP000907304 abstract figure 3</p> <p style="text-align: center;">---</p>	8,11,12
X	<p>SAMPSON B A ET AL.: "Neisseria meningitidis encodes an FK506-inhibitable rotamase"</p> <p>PROC. NAT'L. ACAD. SCI. USA, vol. 89, no. 4, 15 February 1992 (1992-02-15), pages 1164-1168, XP002138648</p> <p>Note: 100% nt seq identity of bp 278-288 (284-294) with bp 719-729 of SEQ ID NO:1745 (60.5% nt seq identity in 281 bp overlap). abstract figure 2</p> <p style="text-align: center;">---</p> <p style="text-align: center;">-/--</p>	8,11,12

INTERNATIONAL SEARCH REPORT

International Application No

PL /US 99/09346

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	HACKER J ET AL.: "Immunophilins: structure-function relationship and possible role in microbial pathogenicity." MOLECULAR MICROBIOLOGY, vol. 10, no. 3, November 1993 (1993-11), pages 445-456, XP000907321 abstract	13,14,17
X	--- DATABASE EMPRI1 [Online] EMBL ID ECUW93, AC U14003 (partial), 30 November 1994 (1994-11-30) BURLAND V ET AL.: "Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes" XP002138657 Note: 100% nt seq identity of bp 37827-37839 with bp 1186-1174 of SEQ ID NO:2791. page 4 -----	8,11,12

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 99/09346

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
1,3,16,18 (all completely); 2,4-15,17 (all partially). Inventions searched:
#1 (SEQ ID NOs 2789/2790), #2 (1/2), #222 (441/442), #246 (489/490), #602 (1201/1202), #729 (1455/1456), #874 (1745/1746), #1397 (2791/2792)
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1. Claims: 1,3,16,18 (all completely); 2,4-15,17 (all partially)

A protein comprising the amino sequence of SEQ ID NO:2790 or comprising a fragment of at least 7 (preferably consecutive) amino acids of said SEQ ID NO; a protein with 50% or greater homology to said protein(s); an antibody binding to said protein(s); a nucleic acid encoding said protein(s), preferably comprising the nucleotide sequence of SEQ ID NO:2789 or a fragment comprising 10 or more consecutive nucleotides thereof; complementary nucleic acid molecules; compositions comprising said protein(s), nucleic acid(s) or antibody for vaccination, diagnosis or pharmaceutical use, preferably immunogenic compositions comprising said protein(s), and the use of said composition(s).

Invention 2. Claims: 2,4-15,17 (all partially)

A protein comprising an amino sequence according to SEQ ID NO:2 or comprising a fragment of at least 7 consecutive amino acids of said SEQ ID NO; an antibody binding to said protein(s); a nucleic acid encoding said protein(s), preferably comprising a nucleotide sequence according to SEQ ID NO:1 or a fragment comprising 10 or more consecutive nucleotides thereof; complementary nucleic acid molecules; compositions comprising said protein(s), nucleic acid(s) or antibody for vaccination, diagnosis or pharmaceutical use, preferably immunogenic compositions comprising said protein(s), and the use of said composition(s).

Inventions 3-1510. Claims: 2,4,-15,17 (all partially)

Same as invention 2 but for proteins limited to the even-numbered SEQ ID NOs:4-3020 except 2790, and for nucleic acids limited to the corresponding odd-numbered SEQ ID NOs:3-3019 except 2789. E.g., invention 3: limited to SEQ ID NO:4 and SEQ ID NO:3, invention 4: limited to SEQ ID NO:6 and SEQ ID NO:5, ... , invention 1509: limited to SEQ ID NO:3018 and SEQ ID NO:3017, and invention 1510: limited to SEQ ID NO:3020 and SEQ ID NO:3019.

INTERNATIONAL SEARCH REPORT

form 1 patent family members

International Application No

PCT/93 99/09346

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
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